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March 14, 2003, 14:23:06; Search time 11.0618 Seconds (without alignments) 476.116 Million cell updates/sec
                                                                                                                                                                                                                         902
1 MNKLLIFVLATFCVFSSFAQ......DVAMGQSSALGFELSFKKSY 179
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                   262574 seqs, 29422922 residues
                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                        US-09-508-487-19
                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                   Sequence:
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inimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

262574

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/pcada.pcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	80	8.9	243	4	US-09-134-001C-2961	Sequence 2961, Ap
~	77.5	9.0	392	4	US-09-071-035-260	بم
٣	77.5	٠	513	4	US-09-291-922-20	20, 7
4	77.5	8.6	1638	4	US-09-071-035-258	258
2	77.5		1638	7	US-09-071-035-262	262,
9	77.5	•	1638	4	US-09-071-035-266	266,
7	74.5		222	4	US-09-134-001C-3521	3521,
æ	72	8.0	332	П	US-08-118-270-53	53,
σ	72	8.0	332	Ŋ	PCT-US93-08528-53	53,
10	71.5	7.9	300	4	US-09-134-001C-4385	4385
11	71.5	-:	303	4	US-09-134-001C-3009	3009,
12	71.5		655	4	US-09-134-001C-5531	5531,
13	71.5	-:	828	4	US-09-255-829-22	22, Ap
14	71.5	7.9	828	4	US-09-255-829-29	29,
15	71.5		1169	4	US-09-255-829-20	20,
16	71		266	7	US-08-225-480-7	7, 1
17		•	266	7	US-09-097-759-4	4,
18		٠	266	4	US-09-118-445-7	7
19		7.9	299	7	US-09-097-759-3	ω,
20	71	٠	306	7	US-09-097-759-2	Sequence 2, Appli
21	70.5	•	402	٦	US-08-314-309A-6	9
22	70.5	•	441	-	US-08-314-309A-4	4
23	70.5	٠	969	4	US-07-757-342D-4	4
24	70	•	349	4	US-09-134-001C-4004	400
25	70		612	m	US-09-295-186-16	٦
26	69.5	7.7	477	4	US-09-134-001C-3487	3487
27	69	7.6	269	ч		'n

RESULT 2
US-09-071-035-260
US-09-071-035-260
Sequence 260, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICAMT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Science, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STREET: 9420 Karyland
COUNTRY: USA

ZIP: 20850

120 VIMAVIRLIEIILPFIFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSA-LGFELSFKK 177

73

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us-09-508-487-19.rai

92

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APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome
                                                                                     63 SFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVVTM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 GSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVVTMAVTRLTEII 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 ANDSKN-----GAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFGIGSFAQGDILG-- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59; Indels 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HV Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
132 LPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.6%; Score 77.5; Di
Best Local Similarity 27.7%; Pred. No. 5;
Matches 43; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: A. Anders Brockes
REGISTRATION NUMBER: 36,373
REFERENCE/CDOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                Sequence 258, Application US/09071035 Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (301) 309-8504
TELEPRAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1638 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071'-035-258
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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US-09-071-035-258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ANDSKN-----GAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFGIGSFAQGDILG--71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.6%; Score 77.5; DB 4; Length 513; Best Local Similarity 26.0%; Pred. No. 0.98; Matches 32; Conservative 18; Mismatches 30; Indels 4
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APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: BB-1163
CURRENT APPLICATION NUMBER: US/09/291,922
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 60/083,044
EARLIER FILING DATE: April 24, 1998
NUMBER OF SED ID NOS: 30
SOFTWARE: Microsoft Office 97
          MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/071,035 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 LPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Mismatches
                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 260:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/09291922 Patent No. 6383776 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  392 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 27.7%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-071-035-260
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5-09-291-922-20
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RESULT 5

3 KLLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFGIG 62

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Sequence 262, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: 611 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
CORRESPONDENCE 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 ANDSKN-----GAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFGIGSFAQGDILG-- 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.6%; Score 77.5; DB 4; Length 1638; 27.7%; Pred. No. 5; tive 22; Mismatches 59; Indels 31
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 LP-----VKGTVNVAVSGALPL--LAVGGS 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                               ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: A Anders Brookes
RECISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: DB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 262:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 266, Application US/09071035 Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1638 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                20850
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-071-035-266
                                                                                                                                                                                                                            COUNTRY:
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Sequence 3521, Application US/09134001C
| Sequence 3521, Application US/09134001C
| Sequence 3521, Application US/09134001C
| Patent No. 6380370
| GENERAL INFORMATION:
| APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REFERENCE: GTC-007
| CURRENT APPLICATION NUMBER: US/09/134,001C
| CURRENT FILING DATE: 1998-08-13
| PRIOR FILING DATE: 1997-11-08
| PRIOR FILING DATE: 1997-11-08
| NUMBER: US 60/055,779
| NUMBER OF SEQ ID NOS: 5674
| SEQ ID NO 3521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.6%; Score 77.5; DB 4; Length 1638; Best Local Similarity 27.7%; Pred. No. 5; Matches 43; Conservative 22; Mismatches 59; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 LPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.3%; Score 74.5; DB Best Local Similarity 25.2%; Pred. No. 0.69; Matches 35; Conservative 17; Mismatches
                                                                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3521
                                                                                                                                                                                                                                                                                                                                                     NAME: A. Anders Brookes
REGISTRATION UNDABER: 36,373
REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEFONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 266:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1638 amino acids
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-134-001C-3521
                                                                                                                                                                                                  FILING DATE:
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89 GAYLDIKALDGITKKAAFQWTWGKGVMLAGVVTMAVTR---LTEIILPFTFANSYNRKLK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 ALDGITK----KAAFQWTWGKGVMLAGVVT-----MAVTRLTEIIL----PFTFANSYNR 142
                                                                                                                                                                                                                                                              Sequence 53, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 LLVYETSKODPIVP-FLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 LFVLLTSRYKLTVPRFIMNL-----SFA------DFCMLYLLL-----IA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 332;
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                        E: BROWDY AND NEIMARK 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 72; DB 28.7%; Pred. No. 2.4; tive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MURPHY-2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/943,236 FILING DATE: 10-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 K--LKNSLNVALGGFEPSFDVAM 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: WUI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Townsend, Kevin G. REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248633
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      ||:| :|| :|| 146 -SLSVIIGGIRIALVVAIG 163
                                                                                                                                146 NSLNVALGGFEPSFDVAMG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: BPIDERAIDS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERRACE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILLNG DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
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TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 ALDGITK----KAAFQWTWGKGVMLAGVVT-----MAVTRLTEIIL----PFTFANSYNR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 LLVYETSKODPIVP-FLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 LFVLLTSRYKLTVPRFIMNL-----SFA------DFCMLYLLL----IA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/08528 FILING DATE: 09-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MURPHY=2 PCT TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.0%; Score 72;
Best Local Similarity 28.7%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4385, Application US/09134001C Patent No. 6380370
RESULT 9
PCT-US93-08528-53
Sequence 53, Application PC/TUS9308528
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 K -- LKNSLNVALGGFEPSFDVAM 163
                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Townsend, Kevin G. REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 10-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERA: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARATERISTICS:
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                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                              Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                         RY: USA
20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-134-001C-4385
                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                CITY: V
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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Matches
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PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14

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70 LGGSLILGFDAVGIGLILAG---AYLDIKALDGITKKAAFQWTWGKGVMLAGVVTMAVTR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|| | : : :| | | :| | | 391 VGGMLAISGESGEIGGIIAGFLAGYL-TQGIKYITRKLPQAIEGLKPTLIYPLLSVSITG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 LTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSALGFELSFKKS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           450 LLMVYVFNPPAAWLNHLLLNGLNSLSGSNIMLLGLVIGAMMAIDMGGPFNKA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Gouler, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN, & FOX F
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/255,829 FILING DATE: 23-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus epidermidis US-09-134-001C-5531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/09255829 Patent No. 6461617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.9%
Best Local Similarity 24.4%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                 RESULT 12
US-09-134-001C-5531
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APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERALIDE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION UNMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-108-14
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                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                 177 IGTVSASEFFVTSSAALSFIIFLGVTQINWFAVIALSLGGMVAAPISAYLVKVLFI---- 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 DG-----ITKKAAFQWIWGKGV-----MLAGVVIMAVTRLTEIILPFTFAN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 GIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVVTMAV----TRLTEIILPFTFA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 MNPLMVFMLWVLLGWKVAIVYFIVLAIFSIFTGLVFSKMNLAESYKGVNVKGDGFFANKE 167
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                34 GEKLLVYETSKQDP---IVPFLINLFLGFGIGSFAQGDI-----LGGSLILGFDAV 81
                                                                                                                                                                                                                                                                                                                                                                                                               ----ILGGSLILGF-DAVGIG-----LILAGAYLDIKAL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SFAQANDSKNGAFGMSA 33
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                                                                                                                                                                                                Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.9%; Score 71.5; DB 4; Length 303; 21.0%; Pred. No. 2.4;
                                                                                                                                                       DB 4; Length 300;
                                                                                                                                                                                                                                                                                                                        44 -----KQDPI-----VPFLLNLFLGFGIGSFAQGD------
                                                                                                                                                                                                                                      1 MNKLLIFVLATFCVFSSFAQANDSKNG-AFGMSAGEKLLVYETS-
                                                                                                                                                                                             67;
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                                                                                                                                                   7.9%; Score 71.5; Di
18.8%; Pred. No. 2.4;
ative 30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3009
                                                                                ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Conservative
                                                                                                                                                                                             51; Conservative
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4385
LENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                   Query Match
Best Local Similarity
Matches 51; Conserv
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                                                                   TYPE: PRT
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P.L.L.C.

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Sequence 531, Application US/09134001C
FRENEAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.9%; Score 71.5; E 24.4%; Pred. No. 7; tive 29; Mismatches
138 NSYNRKLKNSLNVAL 152
                                               274 KLFKKKFVVSFVIAI 288
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138 NSYNRKLKNSLNVALGGFEPSFDVAMGOS 166
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1169 amino acids
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REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                           : 858 amino acids
amino acid
                                                                                                                                                                     Best_Local Similarity 21.59
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 21.5
Matches 32; Conservative
      SEQUENCE CHARACTERISTICS
                                                                                      protein
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COMPUTER READABLE FORM:
                                                                   linear
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                                                                                    MOLECULE TYPE:
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STREET: 11
                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                         Length 858;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/255,829
FILING DATE: 23-FEB-199
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997
PRIOR APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                               56;
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Patent No. 6461617
GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   Ouery Match 7.9%; Score 71.5; DB Best Local Similarity 21.5%; Pred. No. 10; Matches 32; Conservative 30; Mismatches
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    US 08/782,893
                                                         REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 156
TELECOMMUNICATION:
TELEPHONE: 202-371-2600
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REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 151
TELECOMMUNICATION:
TELEPHONE: 202-371-2600
                                                                                                                                                            TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US 0 FILLING DATE: 27-DEC-1996 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-09-255-829-22
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MEDIUM TYPE: Floppy
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ZIP: 20005-3934
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7.9%; Score 71.5; DB 4; Length 858; 21.5%; Pred. No. 10;
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F: 1100 NEW YORK AVENUE, NW, SUITE 600
WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/09255829
Patent No. 6461617
GENERAL:INFORMATION
APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                               30; Mismatches
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21.5%; Pred. No. 16;
Live 30; Mismatches
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Search completed: March 14, 2003, 14:27:42 Job time : 14.0618 secs (Oldsu) Alleran -

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US-09-178-973B-7 US-09-178-973B-7 US-09-354-243B-7 US-09-178-973B-8 US-09-419-568F-8 US-09-354-243B-8 US-09-134-001C-1749 US-08-143-219-27 US-08-143-219-27

US-08-998-416-538

US-08-270-581-1 US-09-146-893-1 US-08-723-306-5 PCT-US96-10041-5

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Sequence

US-08-633-993A-30

ALIGNMENTS

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                                                                    March 14, 2003, 20:13:37; Search time 29.7835 Seconds
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/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
         GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-48-878-7
US-08-750-494-7
US-08-991-677-11
US-08-473-553A-1
US-09-122-4008-5
US-09-122-4008-5
US-08-936-165A-103
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PCT-US95-07721-5
US-09-056-075-1
US-07-867-106-2
US-08-262-220-7
                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                441362 segs, 153338381 residues
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                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                  IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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length: 2000000000
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NAME/KEY: misc_feature
COGATION: 3770.4013
OTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit) from
OTHER INFORMATION: plasmid RP4"
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                                                                                                                                 APPLICANT: Rood, Julian
TITLE OF INVENTION: Expression System for Clostridium
TITLE OF INVENTION: Species
NUMBER OF SOUDENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44.8; DB 2;
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 960296.95238
REFERENCE/DOCKET NUMBER: 960296.95238
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/056,075 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                              ADDRESSEE: Owarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
US-09-056-075-1/c; Sequence 1, Application US/09056075; Patent No. 5955568; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                          APPLICANT: Johnson, Eric A. APPLICANT: Bradshaw, Marite APPLICANT: Rood, Julian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 6243 base pairs
nucleic acid
EDNESS: double
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Best Local Similarity
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Sequence 11, Appl Sequence 1, Appli Sequence 5, Appli Sequence 103, Appli Sequence 7, Appli Sequence 59, Appli Sequence 59, Appli

, Appl , Appl Appli Appl

US-08-680-726A-59

39.

Sequence Sequence Sequence

US-08-680-726A-51 US-08-680-726A-52 US-09-092-409-59 US-09-410-028-3 US-08-451-715A-7

Sequence Sequence Sequence Sequence Sequence

US-08-954-441-1 US-08-617-860B-32 US-08-605-106-4

08-323-170B-1

10592 10592 10592 10592 1648 9636 9636 1850 4098

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Scavenger Receptor Class ČI."
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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APPLICATION NUMBER: US/08/265,428
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TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: PADST, PATERA L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MI
                                                                                             Query Match 5.8%;
Best Local Similarity 46.7%;
Matches 141; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
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STATE: Georgia
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US-08-265-428-5/c
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                                                         US-09-241-581B-5
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                                                           74 ATAATTTGAAAAAAGTTAAATTTAAATAACTTTAAAAAACCTTTTTAAATTTCATTAATA 133
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   4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: Class BI and CI Scavenger Receptors
NUMBER OF SEQUENCES: 8
 Mismatches 157; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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STREET: 2800 One Atlantic Center
1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/241,581B
FILING DATE: 02-Feb-1999
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09241581B Patent No. 6350859 GENERAL INFORMATION:
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STRANDEDNESS: double
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OTHER INFORMATION:
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
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 Conservative
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COUNTRY: USA
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Matches 153;
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1538 ATCATTATTGTTGTTTTTTTTTGTAAACACATTTATTGTAGTTGTTGTTGTTGTTGTTGTTT 1479
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                                                                                                                                                 Length 2032;
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0; Mismatches 161; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Patent No. 6429289
GENERAL INFORMATION:
APPLICANT: Krieger, Monty
TITLE OF INVENTION: Class BI Scavenger Receptors
                                                                                                                                                           DB 4;
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1100 Peachtree Street, Suite 2800
                                                                                                                                                        Score 44.4; DB Pred. No. 0.21;
for the Drosophila Melanogaster
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Gaps

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1418 GGCTTCGGCGTTGTTGAAGTTGTCGCTTTTTTAGTGGTTGTTGTTGTTGTTGTAGTT 1359
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46.7%; Pred. No. 0.21;
ilve 0; Mismatches 161; Indels 0
                                                                                                                             /Function = "Nucleotides 40 through 1926 encode the amino acid sequence for the Drosophila Melanogaster scavenger Receptor Class CI."
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TITLE OF INVENTION: Expression System for Clostridium
TITLE OF INVENTION: Species
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION.
ATTORNEY FAGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Johnson, Eric A.
APPLICANT: Bradshaw, Marite
APPLICANT: Rood, Julian
                                                                                  NAME/KEY: misc. feature
LOCATION: 40..1926
OTHER INFORMATION: /Fun
OTHER INFORMATION: 1926
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Matches 141; Conservative
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ZIP: 53701-2113
COMPUTER READABLE FORM:
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OTHER INFORMATION:
MOLECULE TYPE: HYPOTHETICAL:
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                                           ANTI-SENSE:
FEATURE:
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US-09-056-075-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 ATAGGCTCCTTTGCTCAAGGAGATATTCTTGGAGGTTCTCTTATTCTTGGATTTGATGCG 409
                                                                                                                                                                                                                                       170 ATGAATAAACTTTTAATTTTTGTTTTGGCAACCTTTTGTGTTTTTTCTAGCTTTGCTCAA 229
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                                                                                                                                                5.8%; Score 44.4; DB 4; Length 2032;
46.7%; Pred. No. 0.21;
tive 0; Mismatches 161; Indels 0
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GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: Class BI and CI Scavenger Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 5:
                                      NAME/KEY: misc. feature
COCATION: 40..1926
CTHER INFORMATION: /Func
US-08-265-428-5
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LENGTH: 2032 base pairs
                                                                                                                                                                         Best Local Similarity 46.7
Matches 141; Conservative
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
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: USA
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STATE: Georgia
COUNTRY: USA
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ANTI-SENSE:
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ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
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TELECOMMUNICATION INFORMATION
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                  5.5%;
                       INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2547 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
        215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                   CDS
2378..5038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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Best Local Similarity
Matches 89; Conserva
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                                                                                                                                        linear
                                                                                                                                    TOPOLOGY: line
MOLECULE TYPE: D
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-262-220-7/c
                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                       ; LOCATION:
US-07-867-106-2
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        TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 AAATAACTITAAAAACCITITITAAATTICATTAATATGCTACCATAGTACCAGTTITAA 156
                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 3770..4013
OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from
OTHER INFORMATION: plasmid RP4"
                                                                                                                                                                                                                                                                                                                                                                                                                        37 AAATCAAGAAGCTCTATTGGGAAGCGAATTTCAAGCAATAATTTGAAAAAGTTAAATTT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                            DB 2; Length 6243;
                                                                                                                                                                                                                                                                                                                                        Query Match 5.7%; Score 43; DB 2; Length 624 Best Local Similarity 49.8%; Pred. No. 0.5; Matches 109; Conservative 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1445 TATAATCTTTGAAGAAAAATATAAAAATGAGCCTTT 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 TAGCTTTGCTCAAGCTAATGATTCTAAAAATGGTGCGTT 255
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: RICE-0002 TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6243 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                           132 TATGCTACCATAGTACCAGTTTTAATAAAGGGGTTTTTTATGAATAAACTTTTAATTTTG 191
                                                       Gaps
     Length 5852;
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                                                                                                                                                                                                                                                                                                                   192 TITIGGCAACCTITIGIGITITITICIAGCTTTGCTCAAGCTAATGATT 239
                                                  79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BERGSTROM SVEN
APPLICANT: BARBOUR ALAN G.
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH STREET, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/262,220
FILING DATE: 20-JUN-1994
CLASSIFICATION: 514
     DB 1;
Score 41.6; D
Pred. No. 1;
0; Mismatches
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74 ATAATTIGAAAAAGTTAAATTTAAATAACTTTAAAAACCTTTTTAAAATTTCATTAATA 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08468878
Patent No. 6090586
GENERAL INFORMATION:
APPLICANT: BERGSTROM SVEN
APPLICANT: BARBOUR ALAN G.
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20004
COUNTRY: USA
ZIP: 20004
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,878
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/262,220
FILING DATE: 20-JUN-1994
ATTORNEY/AGENT INFORMATION:
ANAL: ACCORDED
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                  Score 41.4; DB 3;
Pred. No. 0.97;
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                                         STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Borrlia garinii
STRAIN: IP90
                                                                                                                                                                                                                                                                                                                                                                                       5.5%;
              LENGTH: 2547 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 117; Conservative
 SEGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               sig_peptide
380..442
                                                                                                                                                                                                                                                                                                                  mat_peptide
443..2242
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                                                                                                                                                                                                              CDS
380..2245
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: pJB-101
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                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                            LOCATION:
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                                                                                                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2547;
                                                                                                                                                                                                                                                                                                              0; Mismatches 106; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: BERGSTROM SVEN
APPLICANT: BERGSTROM ALAN G.
TITLE OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: TEAPOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,733
FILING DATE: 06-JUN 1995
PRIOR APPLICATION NUMBER: 08/262,220
FILING DATE: 20-JUN 1994
ATTONNEY/AGENT INPORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
                                                                                                                                                                                                                                                                            Score 41.4; DB 3;
Pred. No. 0.97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: BERGSTROM-3 FELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BROWDY AND NEIMARK STREET: 419 SEVENTH STREET, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-08-471-733-7/c
; Sequence 7, Application US/08471733
; Patent No. 6068842
                                                                                                                                                                                                                                                                          Query Match 5.5%;
Best Local Similarity 52.0%;
Matches 117; Conservative
                Borrlia garinii
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                     sig_peptide
380..442
                                                                                                                                                                                                        mat_peptide 443..2242
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                                                                                                  CDS
380..2245
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ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                             IMMEDIATE SOURCE:
CLONE: pJB-101
ORIGINAL SOURCE:
                                Ip90
                                                                                                                                                                                                     NAME/KEY:
COCATION:
US-08-262-220-7
                                                                                                  NAME/KEY:
                                                                                                                                                                      LOCATION:
FEATURE:
                ORGANISM:
STRAIN: 1
                                                                                                                    LOCATION:
                                                                                                                                                     NAME/KEY:
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134 TGCTACCATAGTACCAGTTTTAATAAAGGGGTTTTTATGAATAAACTTTTAATTTTTGTT 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 TATTATTATTATTATTTTTATTATTATTCAAATCTATAAATAA - GATTAATTTTATTG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer. Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617
CURRENT APPLICATION NUMBER: US/08/991,677A
CURRENT FILING DATE: 1997-12-16
EARLIER FILING DATE: 1996-12-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41.4; DB 4; Length 2547;
Pred. No. 0.97;
0; Mismatches 106; Indels 2
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                                                                                                                          BERGSTROM=3
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                           APPLICATION NUMBER: 08/262,220
                                                                            REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: BERG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.5%;
                                                                                                                                                                                             TELEX: 248633
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 2547 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Borrlia garinii
                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 52.0
Matches 117; Conservative
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443..2242
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380..442
                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                         TOPOLOGY: linea
MOLECULE TYPE: DN
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: pJB-101
                                                                                                                                                                                                                                                                                                                                                                                          Ip90
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LOCATION:
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; LOCATION:
US-08-750-494-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 TIGGCAACCTITIGIGITITITICIAGCITIGCICAAGCIAAIGAIICIAAAAAIGGIGCG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.5%; Score 41.4; DB 3; Length 2547; 52.0%; Pred. No. 0.97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 TITGGGATGAGTGCTGGAGAAAACTTTTGGTTTATGAAACTAGC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08750494
Patent No. 6204018
GENERAL IO. 6204018
GENERAL BERGSTROM SVEN
APPLICANT: BERGSTROM SVEN
APPLICANT: BARBOUR ALAN G.
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 106;
REFERENCE/DOCKET NUMBER: BERGSTROM=3
TELECOMMUNICATION INFORMATION:
TELEPAN: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 7:
SEOUBNCE CHARACTERISTICS:
LENGTH: 2547 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS; double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BROWDY AND NEIMARK STREET: 419 SEVENTH STREET, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
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                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 52.0
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide 443..2242
                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
380..442
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380..2245
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                      STRAIN: IP90
IMMEDIATE SOURCE:
CLONE: pJB-101
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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US-08-468-878-7
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LOCATION:
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US-08-473-553A-1
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Best Local 8
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                FEATURE:
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                                                                                                                                                                                                              121 AATTTCATTAATATGCTACCATAGTACCAGTTTTAATAAAGGGGTTTTTATGAATAAACT 180
                                                                                                                                                                                                                                                                            619 ACTATAAATTGAGTTGTGAATGAGTGTTTTATGGATTTTTAAGATGTTAAATTTATATA 678
                                                                                                                                                                                           61 CGAATTTCAAGCAATAATTTGAAAAAGTTAAATTTAAATAACTTTAAAAACCTTTTTAA 120
                                                                                                                                                                                                                                                                                                                                                    1 ATTGTTAAAAGAATTGAAATTGATAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAG 60
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                                                              Length 2251;
                                                                                            0; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
ATOONEY/AGENT INFORMATION:
NAME: $11va, Robin M.
REGISTRATION NUMBER: 38,304
REPRENCE/DOCKET NUMBER: A-60886/RFT/RMS
TELECOMMUNICATION INFORMATION:
                                                                              1.3;
                                                            Query Match 5.4%; Score 40.8; Best Local Similarity 48.0%; Pred. No. 1... Matches 117; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/08473553A; Patent No. 5859338; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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94111-4187
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CITY: San Francisco
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
          ; ORGANISM: Pinus taeda
US-08-991-677-11
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1153 AAAGTCCAAACCGATCAAATTAATAGCAACTGCCGATACCAAATTATATTCGTTTTGTAA 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1033 AAATCACTAGTTTGAAACTAAAGGTACTAAAAAACTATTTAATGTTTGAAGTTTTAGGTTT 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      613 AGAAGAAAATATTTTTTTTTTA--GTTTTTACAAAAATATTGTTTTAGAAAATATTTTCA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 GTTTTTAGTAGTTTTTTCCAGATTTTACAAATAAAATTGCTTTAGAAAATTGATTTTCAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 TITCAAGCAAIAAITIGAAAAAGTIAAAFIIIAAAIAACIIITAAAAACCIITITAAAAII 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   673 TTTCTAAAGTAATTAAAAACTGGAAAAACTTAAATTTTTTAACTAAAAAACTGAAAAAA 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATCCTATTGTACCATTTTTATTGAACCTTTTTTTAGGGTTTGGAATAGGCTCCTTTGCT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                       10 AGAATTGAAATTGATAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAGCGAATTTCA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 TTAAAAGAATTGAAATTGATAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAGCGAA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                          130 AATATGCTACCATAGTACCAGTTTTAATAAGGGGGTTTTTATGAATAAACTTTTAATTTT
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                                                                                       Length 5733;
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                                                                                 Score 40.8; DB 2; Length 5
Pred. No. 1.5;
0; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 200; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Michalowaki, Susan
APPLICANT: Spiker, Steven
TITLE OF INVENTION: MATRIX ATTACHMENT REGIONS
FILLE REFERENCE: Michalowaki and Spiker
CURRENT APPLICATION NUMBER: US/09/122,400B
CURRENT FILING DATE: 1998-07-24
PRIOR PILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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US-09-122-400B-5/c
; Sequence 5, Application US/09122400B
· Patent No. 6245974
                                                                                    5.4%;
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                                                                                                                                           Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 172; Conservative
5117..5467
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                                                                                                               Similarity
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22,592
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SEQUENCE CHARACTERISTICS:
FROGH: 2973 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 49.5
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid_
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                      Lexington
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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219..2834
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                                                                                                                                                            RESULT 15
US-08-451-715A-7/c
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; LOCATION:
US-08-451-715A-7
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94 TITAAATAACTITAAAAACCITITITAAATITCAITAATAGCTACCATAGTACCAGTIT 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624 ACAATCAATTTAATTTCTTAANTAAATTTGTACTTATTATTATGTTGCATTATTTTTAT 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    684 TTCAAATAAATAATTAATTATNTTGNATATTTCTCTTTNACGTTACCANAATATACATAT 625
                                                                                                                                                                                                                                                                                                                                                                    No. 6348582el Prokaryotic Polynucleotides,
Polypeptides and Their Uses
534
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Pred. No. 1.8;
0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/936,165A FILING DATE: 24-SEP-1997
                                                                                                                                                          Application US/08936165A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY,AGENT INFORMATION:
NAME: Gimmi, Edward R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         Black, Michael
Burnham, Martin
Hodgson, John
Knowles, David
Lonetto, Michael
                                                                                                                                                                                                                                                                                         Nicholas, Richard
                                                                                                                                                                                                                                                                                                    Pratt, Julie
Reichard, Richard
                                                                                                                                                                                                                                                                                                                                      Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.2%;
Best Local Similarity 46.7%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: Genomic DNA
US-08-936-165A-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 796 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 709 STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                            365 CAAGGAGATATTCT 378
                                                                            375 AAAATAGTTTTTT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ward, Ju
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Black,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                           RESULT 14
US-08-936-165A-103/c
; Sequence 103, Applic
; Patent No. 6348582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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APPLICANT:
APPLICANT:
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Patent No. 5801013
GENERAL INFORMATION:
APPLICANT: Tao, Jianshi
APPLICANT: Houman, Fariba
APPLICANT: Shen, Xiaoya
APPLICANT: Shen, Xiaoya
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: Helicobacter Aminoacyl-tRNA Synthetase
TITLE OF INVENTION: Proteins, Nucleic Acids and Strains Comprising Same
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                    564 TATTGTTTCATTTGAGNTAAACCCTTTTTGAAATCAAGGTTTTAGTAGGAAAAATCCATA 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 TIGAAAAAAGTIAAATITAAATAACTITAAAAACCTTTTTTAAAATTTCATTAATATGCTA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 AAATAGAGCGTTCTTTCAAAAATGGTTGAATTTGGAACGCCTTTTGCTTTTACGTTTTA 143
214 TTCTAGCTTTGCTCAAGCTAATGATTCTAAAAATGGTGCGTTTGGGATGAGTGCTGGAGA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 ATTGATAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAGCGAATTTCAAGCAATAAT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2973;
                                                                                                                                                           504 AACCCCGGTTTTNAAGANTAATTGCATTTNAGCNAATATTGTCAGTTT 456
                                                                                                            274 AAAACTTTTGGTTTATGAAACTAGCAAGCAAGATCCTATTGTACCATTT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,715A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39.2;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISFRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CPI:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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OY 199 AACCTTTGGGTTTTTCTAGCTT 222 | | | | | | | | | | | | | | Db 142 ATTGTGGGTATTTTTCAAART 119 Search completed: March 15, 2003, 07:43:26 Job time : 60.7835 secs (OT48U) NWAJE BLANK (USPTO)

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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nucleic search, using sw model OM nucleic -

March 14, 2003, 22:48:52 ; Search time 49.6392 Seconds
(without alignments)
10731.744 Million cell updates/sec Run on:

US-09-508-487-18 759 Perfect score:

1 attgttaaaagaattgaaat......attctgtattgaaatgggtg 759 IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

501302 seqs, 350932545 residues Searched:

1002604 Total number of hits satisfying chosen parameters:

Inimum DB seq length: 0

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

Published_Applications_NA:*

// Cgn2_6/ptodata/2/pubpna/USO7_pUBCOMB.seg:*
// Cgn2_6/ptodata/2/pubpna/DSO6_NEW_PUB.seg:*
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// Cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seg:*
// Cgn2_6/ptodata/2/pubpna/DSO7_NEW_PUB.seg:*
// Cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seg:*
// Cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seg:*
// Cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seg:*
// Cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seg:*
// Cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seg:*

/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dР				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
-	51.2	6.7	416	10	US-09-960-352-4584	Seguence 4584. Ap
2	46		640681	10	115-09-790-988-1	Segmence 1 Appli
m	45.6	9	2000	6	US-09-938-842A-5061	Sequence 5061. An
4	44.2	2.8	513509	6	US-09-754-853A-4	Sequence 4, Appli
2	43	5.7	3979	Φ	US-09-989-919-52	Sequence 52, Appl
9	42.2	5.6	419	10	US-09-960-352-11234	Sequence 11234, A
7	42	5.5	5520	Φ	US-10-001-887-43	Sequence 43, Appl
8 0	41.8	5.5	337	10	US-09-960-352-6036	Sequence 6036, Ap
6	41.4	5.5	2846	6	US-10-008-016-1	Sequence 1, Appli
c 10	41	5.4	640681	10	US-09-790-988-1	Sequence 1, Appli
11	40.8	5.4	431	10	US-09-969-373-739	Sequence 739, App
12	40.8	5.4	2251	10	US-09-796-256A-11	Sequence 11, Appl
13	40.8	5.4	127197	6	US-09-754-853A-1	Sequence 1, Appli
14	40.6	5.3	352	10	US-09-960-352-10129	Sequence 10129, A
15	40.6	5.3	414	10	US-09-960-352-6528	Sequence 6528, Ap
c 16	40.6	5.3	2846	6	US-10-008-016-1	Sequence 1, Appli
17	40.6	5.3	20966	10	US-09-776-976-7	Sequence 7, Appli
18	40.6	5.3	20966	10	US-09-758-055-7	Sequence 7, Appli
19	40.6	5.3	20966	10	US-09-909-547-7	Sequence 7, Appli

444	Sequence 2276, Ap Sequence 1405, Ap Sequence 5, Appli	m	Sequence 14521, A Sequence 4370, Ap Sequence 13, Appl	101 -	Sequence 1, Appli Sequence 7661, Ap Sequence 1447, Ap	N N 4 4	sequence 4/84, Ap Sequence 84, Appl Sequence 15, Appl	7, A 10, 35,
	10 US-09-954-456-2276 10 US-09-867-550-1405 10 US-09-816-894-5	D	10 US-09-960-352-14521 9 US-09-938-842A-4370 10 HS-09-773-416-13	D :	5	00	US-09-938-842A-4/84 US-10-081-051-84 US-09-966-880A-15	
		796 1 1674 9 3935 1						2818 9 6564 9 1204 9
		5.22		1.00			22.T	5.1
40.7 40.2 40.2	40.2 40.4	30.08 8.00 8.00 8.00	39.4 39.4	86 80 80 80 80 80 80 80 80 80 80 80 80 80	3888	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	38.6 38.6 38.6	38.6 38.6 38.6
	0 0 0 54 3	c 26 c 27	c 29		ი 33.44	0 38 39	c 41 42	44 44 5

ALIGNMENTS

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US-09-960-352-4584
US-09-960-352-4584
US-09-960-352-4584
Sequence 4584, Application US/09960352
Facent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLER ALD FAND DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICANTION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 4584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 ATTAATATGCTACCATAGTACCAGTTTTAATAAAGGGGGTTTTTATGAATAAACTTTTAAT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 TTTTGTTTTGGCAACCTTTTGTGTTTTTTTTTTGGCTTTGCTCAAGCTAATGATTCTAAAAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 TCAAGCAATAATTTGAAAAAGTTAAATTTAAATAACTTTAAAAACCTTTTAAATTTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AAAAGAATTGAAATTGATAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAGCGAATT 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 416;
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                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 20-LIB3057-016-Q1-K1-E11
US-09-960-352-4584
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 6.7%; Score 51.2; DB 10;
Best Local Similarity 50.8%; Pred. No. 0.093;
Matches 122; Conservative 0; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                   LENGTH: 416
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APPLICANT: Hauge, Brian M.
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jacremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 108907 AATTGATGTTTTAIATTAAAAATTAGATGAAATTCCATCCAAATCTTTTAAAAAATAA 108966
                                                                                                                                                                                                                                                                     1490 AACAACATGTTTATTTTGGTTTTGGTCAACGAATTTTTCATGTTTAAATGGTAGTCAACG 1549
                                                                                                                                                                              1550 TITAGIICAIGIIITAAAIGGCCACAIAIGAACIIGAIGIITAAAAIGGCCACAAITIAA 1609
                                                                                                                                                  93 ATTTAAATAACTTTAAAAACCTTTTTTAAATTTCATTAATATGCTACCATAGTACCAGTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTTTAGGGTTTGGAATAGGCTCCTTTGCTCAGGAGATATTCTTGGAGGTTCTCTTA 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 AATTGATAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAGCGAATTTCAAGCAATAA 77
                                                                                                                                                                                                                                                                                                                                213 TITCIAGCITIGCICAAGCIAAIGATICIAAAAATGGIGCGITIGGGAIGAGIGCIGGAG
                                                                                                                                                                                                                                         153 TIAATAAAGGGGTTTTTATGAATAAACTTTTAATTTTTGTTTTGGCAACCTTTTGTGTTT
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                                                                                                                  Indels
                                                                                                             0; Mismatches 154;
                                                                    Score 45.6; DB 9;
Pred. No. 1.7;
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LOCATION: (111805)..(113968),(114684)..(115204)
LOCATION: (111805)..(113968),(114684)..(115204)
NAME/KEY: unsure
LOCATION: (1)..(513509)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: clone ID: 318013_region_A3
US-09-754-853A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44.2; DE Pred. No. 11; 0; Mismatches
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; ORGANISM: Arabidopsis thaliana US-09-938-842A-5061
                                                                  6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.8%;
Best Local Similarity 51.2%;
Matches 103; Conservative
                                                                Query Match
Best Local Similarity 49.09
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1610 AACTIG 1615
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US-09-754-853A-4
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REPERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US 60/227,866
FRIOR FILING DATE: 2001-08-24
FRIOR FILING DATE: 2001-08-24
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 5061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TITAATITITGTTTTGGCAACCTITTGTGTTTTTTTTTTGTGCTTTTGCTCAAGCTAATGATTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATTGTTAAAAGAATTGAAATTGATAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAG 60
                                                                                                         APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
TILE OF INVENTION: SAKARI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APPLIDS
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR FILING DATE: 2001-04-07
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.1%; Score 46; DB 10; Length 640681; llarity 49.2%; Pred. No. 4.9; Conservative 0; Mismatches 125; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5061, Application US/09938842A
Patent No. US20020160378A1
                                                ; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Buchnera sp
US-09-790-988-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35980 ATTAAA 35985
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                                                                                           GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Sim
Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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APPLICANT: Macina, Soberto
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Liu, Chenghua
TILLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
TILLE REFERENCE: DEX-0269
CURRENT APPLICATION NUMBER: US/10/001,887
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/249,998
PRIOR APPLICATION NUMBER: 60/249,998
PRIOR APPLICATION NUMBER: 60/252,563
PRIOR PILING DATE: 2000-11-22
REPROR FILING DATE: 2000-11-22
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                                                                                                                                                                                                                                                                                                                                                                                    65 TTTCAAGCAATAATTTGAAAAAGTTAAATTTAAATAACTTTAAAAACCTTTTTAAATT 124
                                                                                                                                                                                                                                                                                                                                                       125 TCATTAATATGCTACCATAGTACCAGTTTTAATAAAGGGGTTTTTATGAATAAACTTTTA 184
                                                                                                                                                  5 TTAAAAGAATTGAAATTGATAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAGCGAA 64
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Pred. No. 11;
0; Mismatches 120; Indels
                                                 Length
                                                                                                   Indels
                                                 DB 10;
                                               Score 42.2; DI
Pred. No. 6;
0; Mismatches
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                                                 Query Match 5.6%;
Best Local Similarity 51.3%;
Matches 98; Conservative
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APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
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ORGANISM: Homo sapien
US-10-001-887-43
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JS-09-960-352-11234
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APPLICANT: Recipon, Herve
APPLICANT: Pluta, Jason
APPLICANT: Pluta, Jason
APPLICANT: Chorden
APPLICANT: Chorden
APPLICANT: Liu, Chenghua
APPLICANT: DX-0289
CURRENT APPLICATION NUMBER: US/09/989,919
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/252,505
PRIOR APPLICANT: 2000-11-22
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin version 3.1
SEQ ID NO 52
LENGTH: 3979
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Db 108967 TGCATCAAAATTTGTATATTTTAAATATTAAAAGACTTTTTTATAAGTTATAAAAATT 109026
                                                                         DD 109027 ATAATTGAATACCACCAAATTTTATTATTTTTCTTAAAAAATCTTAAATGTTTTAATTGA 109086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2495 ATTAATAAGCACTCATACTACCAATTATCACTAACTTGCCATTTTTTGTATGCTGTATT 2554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2615 AATTATGGTATATATAGGCGTTGGAAAAAACATTTATATAATGAAAGTATGTAGGGG 2673
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OTHER INFORMATION: Clone ID: 48-LIB3058-052-Q1-K1-D8
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Pred. No.
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                          ; Sequence 52, Application US/09989919; Patent No. US20020114344A1
; Patent No. INFORMATION:
APPLICANT: Macina, Roberto
                                                                                                                                                                                                 Db 109087 ATACCATAAGACTTTTTATA 109107
                                                                                                                                                198 CAACCTTTTGTGTTTTTTCTA 218
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Best Local Similarity 52.5'
Matches 94; Conservative
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US-09-989-919-52
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US-09-989-919-52
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Db 624202 AATAAATAAGCCITTICCICCAATITITGAAAGAGAITTATIAAAAIATTATATATCTCCAIG 624143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATANABE, HASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REPERENCE: 081356/0129
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.4%; Score 41; DB 10; Length 640681;
45.1%; Pred. No. 48;
                                          Length 2846;
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                                                            13;
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                                                                                       Mismatches
                                             5.5%; Score 41.4;
24.8%; Pred. No. 13
tive 55; Mismatches
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                                                                                     Conservative
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                                          Query Match
Best Local Similarity
Matches 30; Conserv
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Matches 152; Conserv
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US-10-008-016-1
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                                                                                                                                                                    APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Magappan
TITLE OF INVENTION: NUCLEIC AGID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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| Patent No. US20020173630A1
| GENERAL INFORMATION:
| APPLICANT: Meyers, Rachel A. APPLICANT: Tsai, Fong-Ying
| TITLE OF INVENTION: 3217, A NOVEL HUMAN AMP-BINDING ENZYME
| TITLE OF INVENTION: TRAMILY MEMBER AND USES THEREOF
| FILE REFERENCE: 10448-110001
| CURRENT FILING DATE: 2001-11-08
| PRIOR APPLICATION NUMBER: 60/246,669
| PRIOR APPLICATION NUMBER: 60/246,669
| PRIOR APPLICATION NUMBER: 60/260,166
| PRIOR FILING DATE: 2001-11-08
| PRIOR FILING DATE: 2001-01-05
| PRIOR FILING DATE: 2001-01-05
| PRIOR FILING DATE: 2001-01-05
| SEQ ID NO 1
| SEQ ID NO 1
| LENGTH: 2846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 5.5%; Score 41.8; DB 10; Best Local Similarity 51.3%; Pred. No. 6.9; Matches 97; Conservative 0; Mismatches 92;
                                                                                 Sequence 6036, Application US/09960352
patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: CDS
LOCATION: (245)...(2299)
NAME/KEY: misc_deature
LOCATION: (1)...(2846)
OTHER INFORMATION: n = A,T,C or G
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                                                          US-09-960-352-6036/c
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LENGTH: 337
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-10-008-016-1
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Sequence 11, Application US/09796256A
; Patent No. US2002007847741
; GENERAL INFORMATION:
    APPLICANT: Carraway, Daniel T
    APPLICANT: Carraway, Daniel T
    APPLICANT: Smeltzer, Richard H
    TITLE OF INFORMATION: Production of Syringyl Lignin in Gymnosperms; FILE REFERENCE: 50617/c-3532.0
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US60/033381
; PRIOR PELING DATE: 1996-12-16
; PRIOR FILING DATE: 1996-12-16
; PRIOR FILING DATE: 1997-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 ACTTTTAATTAAATATTTAATATTTCTTAAAATTTATCATTAAATTCAAAATTCATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 431;
                          GENERAL INFORMATION:

APPLICANT: Effertz, Roger J.

APPLICANT: Effertz, Roger J.

APPLICANT: Hauge, Brian M.

ITILE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A.

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT APPLICATION NUMBER: US 09/754,853

PRIOR APPLICATION NUMBER: US 09/754,853

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 4593

SEQ ID NO 739

LENGTH: 431
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Pred. No. 16;
0; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40.8;
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Sequence 739, Application US/09969373 Patent No. US20020133852A1
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Best Local Similarity 48.0%;
Matches 117; Conservative (
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                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-739
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LENGTH: 2251
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APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Mang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
TITLE OF INVENTION: NUMBER: US/09/754,853A
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1
LENGTH 127197
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                                                                                                                                                                           TITAATTITIGITITIGGCAACCTITIGIGITITITICIAGCTITIGCICAAGCTAATGATIC 240
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US-09-754-853A-1
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; Sequence 10129, Application US/09960352
; Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09754853A Publication No. US20030005491A1
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APPLICANT: Warren, Wesley
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
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APPLICANT: Tao, Mengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REPREMENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 6528
LENGTON.
              TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC AND FAR DEPOSITION
FILLE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: U5/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
FEG ID NO 10129
LENGTH: 352
TYPE: DNA
ORGANISM: BOS TAULUS
ORGANISM: BOS TAULUS
CORGANISM: Clone ID: 44-BOVMS1-003-Q1-E1-C8
US-09-960-352-10129
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OTHER INFORMATION: CLONE ID: 28-LIB3058-032-Q1-K1-G11
US-09-960-352-6528
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47.1%; Pred. No. 13;
tive 0; Mismatches 139;
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5.3%; Score 40.6; DB 10;
Best Local Similarity 49.3%; Pred. No. 12;
Matches 106; Conservative 0; Mismatches 109;
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Mathialagan, Nagappan
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Matches 124; Conservative
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269 GGAGAAAACTTTTGGTTTAIGAAACTAGCAAGCAAGAICCTAITGTACCATTTTTAIIG 328
                               329 AACCTTTTTTAGGGTTTGGAAT 351
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392 TATATTTTTTTTTTTAT

Search completed: March 15, 2003, 14:13:38 Job time: 528.639 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2003, 14:19:56 ; Search time 31.1742 Seconds
(without alignments)
765.116 Million cell updates/sec Run on:

US-09-508-487-19

902 1 MNKLLIFVLATFCVFSSFAQ......DVAMGQSSALGFELSFKKSY 179 Perfect score: sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Inimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_101002:*

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2: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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4: /SIDSI/gcgdata/geneseqy-embl/AA1993.DAT:*
4: /SIDSI/gcgdata/geneseqy-embl/AA1993.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*/SIDS1/gcgdata/geneseq/geneseq-embl/AA1995.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* /SIDS1/gcgdata/geneseg/genesegp-emb1/AA2001.DAT:*/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2002.DAT:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

SOMETHINGS	Description	AAY19808 B. burqdorferi ant			AAY04279 Borrelia afzelii		AAY04282 pll protein seque		AAB88515 Haemophilus influe	AAU91446 Haemophilus influ	10000014
	В ІВ		20 7	20 7	20 7		20 7		22 1	23 1	23
	Query Se Match Length DB 1	179	179	158	178	177	95	25	378	378	255
ď	Query Match	100.0	100.0	88.6	85.3	81.7	17.2	14.2	9.4	4.6	0
	Score	902	902	799	769.5	737	155.5	128	84.5	84.5	0
	Result No.		7	e	4	'n	9	7	80	6	-

Novel human diagno Novel human diagno	tamicum	.glutamicum	glutami	A protein with cat	Mouse OCTN1 amino				О	Streptococcus pneu	u	C glutamicum prote		Salmonella typhi c	0	C glutamicum prote	Corynebacterium gl	C glutamicum prote	Corynebacterium gl	C glutamicum prote		E faecalis EF068 a	tionis m	Corn Beta vulgaris	Enterococcus faeca	s	nterococcu	faecalis EF0	aecalis EFO	faecalis	Micromonospora eve	3] i	Arabidopsis thalia
ABG07111 ABG24514	85	AAB78951	AAB78952	65	27	AAY81595	87	ABP27031	ABP09270	AAU37748	ABP38116	AAG91121	AAB78989	833	AAB76781	AAG93096	AAB76751	AAG92057	AAB76750	AAG93106	AAY00139	ABP43358	AAW99600	AAU97210	3	4	AAY00142	ABP43357	ABP43359	ABP43361	AAU04855	10	AAG53005
22	22	22	22	20	21	21	23	23	23	22	23	22	22	22	22	22	22	22	22	22	20	23	20	23	20	20	20	23	23	23	22	21	21
1456	384	384	369	553	553	572	325	504	111	650	243	487	487	319	345	417	324	346	346	513	392	392	502	513	1638	1638	1638	1638	1638	1638	251	1755	1793
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84 84	3	83.5	82	82	8	81.5	81	81	80.5	ö	80	80	80	6	79.5	6	79	79	79	78.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	^	76.5	9
11	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

Antigenic protein; vaccine; Lyme disease; infection; detection. B. burgdorferi antigenic protein, f933.aa. AAY19808 standard; Protein; 179 AA 97US-0057483. 97US-0050359. 97US-0053344. 97US-0053377. 98WO-US12718 (first entry) Borrelia burgdorferi. 03-SEP-1997; 20-JUN-1997; 22-JUL-1997; 22-JUL-1997; WO9859071-A1. 18-JUN-1998; 19-JUL-1999 30-DEC-1998 AAY19808; AAY19808

(HUMA-) HUMAN GENOME SCI INC. (MEDI-) MEDIMMUNE INC.

Lathigra R; Hanson MS, Erwin AL, Choi GH,

WPI; 1999-189980/16. N-PSDB; AAX61505.

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19-JUL-1999
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                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             AAY19809;
                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                              121
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                                                                              invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a Borrelia burgdorferi B313 protein. The present invention describes an isolated nucleic acid (I) that: (i) encodes a polypeptide fragment (II) immunologically reactive with rabbit polyclonal antibody raised against a 13 kDa polypeptide of Borrelia burgdorferi B313, but not reactive with most proteins from
                                                                                                                                                                                                                                                                                     IGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFOWTWGKGVMLAGVV 120
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                              1 MNKLLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFG 60
                                                                                                                                                                                                                                           TMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSALGFELSFKKSY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid from Borrelia burgdorferi encoding virulence associated
protein P13
                                                                     This sequence represents a Borrelia burgdorferi (Bb) protein of the
products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia; Pl3 antigen; spirochaete; vaccine; infection; diagnosis.
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                                                                                                                                                                                   Length 179;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                  100.0%; Score 902; DB 20; 100.0%; Pred. No. 5.3e-95;
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 31; Page 108-109; 118pp; English.
                                             Claim 12; Page 72; 275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi B31 protein.
                                                                                                                                                                                                                                                                                                                                                                                                AAY04278 standard; Protein; 179
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97DK-0001041.
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                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorrelia burgdorferi
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N-PSDB; AAX30098.
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                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                              179 AA;
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10-SEP-1997;
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                                                                                                                                                                                                        Matches 179;
                                                                                                                                                              Seguence
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to specific nucleic acid sequences but not to genomic DNA from most other spirochaetes. (I), (II) and transformed cells are useful in vaccines to protect against infection by B. burgdorferi sensu lato. (I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi sensu lato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other spirochaetes; and/or (ii) hybridizes under stringent conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNKLLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSALGFELSFKKSY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Borrelia burgdorferi nucleic acids – used to develo products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigenic protein; vaccine; Lyme disease; infection; detection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 902; DB 20;
100.0%; Pred. No. 5.3e-95;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                               compared with use of whole bacteria as antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY19809 standard; Protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanson MS,
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97US-0050359.
97US-0053344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 179; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      179 AA;
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(MEDI-) MEDIMMUNE
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can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a Borrelia afzelii ACAI protein. The present invention describes an isolated nucleic acid (1) that: (i) encodes a polypetide fragment (II) immunologically reactive with rabbit polyclonal antibody raised against a 13 kDa polypeptide of Borrelia burgdorferi B313, but not reactive with most proteins from other spirochaetes; and/or (ii) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most other spirochaetes (I), (II) and transformed cells are useful in vaccines to protect against infection by B. burgdorferi sensu lato. (I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi
                                                                                                                                                                                                                                                                       82 GIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVVTMAVTRLTEIILPFTFANSYN 141
                                                                                                                                                           Gaps
                                                                                                                                                                                         NDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAV 81
                                                                                                                                                                                                         Nucleic acid from Borrelia burgdorferi encoding virulence associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia; P13 antigen; spirochaete; vaccine; infection; diagnosis.
                                                                                                                                                           ;
                                                                                                                          Length 158;
                                                                                                                          Score 799; DB 20;
Pred. No. 2.8e-83;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                   RKLKNSLNVALGGFEPSFDVAMGQSSALGFELSFKKSY 179
                                                                                                                                                                                                                                                                                                                                    Claim 31; Page 111-112; 118pp; English.
                                                                                                             88.6%; Scor
100.0%; Pred
0; N
                                                                                                                                                                                                                                                                                                                                                                                                                               AAY04279 standard; Protein; 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia afzelii ACAI protein.
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                                                                                                                                         st Local Similarity
tches 158; Conserv
                                                                                              158 AA;
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10-SEP-1997;
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                                                                                              Seguence
                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                     142
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The present sequence represents a Borrelia garinii 1P90 protein. The present invention describes an isolated nucleic acid (1) that: (i) encodes a polypeptide fragment (II) immunologically reactive with cabbit polyclonal antibody raised against a 13 kDa polypeptide of Borrelia burgdorferi B313, but not reactive with most proteins from there spirochaetes; and/or (ii) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most to specific nucleic acid sequences but not to genomic DNA from most ovaccines to protect against infection by B. burgdorferi sensu lato.

(I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization fests. (I) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi sensu lato, but is absent from other Borrelia species (e.g. those
sensu lato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis, compared with use of whole bacteria as antigen.
                                                                                                                                                                                                                                                               IGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVV 120
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                   Nucleic acid from Borrelia burgdorferi encoding virulence associated
                                                                                                                                                                                         1 MNKLLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFG
                                                                                                                                                                                                             Borrelia; P13 antigen; spirochaete; vaccine; infection; diagnosis.
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                                                                                                                       Length 178;
                                                                                                                                                         Indels
                                                                                                                       DB 20;
                                                                                                                     85.3%; Score 769.5; DB 284.9%; Pred. No. 7.7e-80;
                                                                                                                                                         10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY04280 standard; Protein; 177 AA
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97DK-0001041.
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                                                                                                                                         Best Local Similarity 84.9 Matches 152; Conservative
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                                                                                     178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia garinii.
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                                                                                       Sequence
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                                                                                                                       Query Match
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AAY04280
   SSSSXS
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The present invention describes an isolated nucleic acid (I) that: (1) encodes a polypeptide fragment (II) immunologically reactive with rabbit polychothal antibody raised against a 13 kba polypeptide of aborella burgdorferi B313, but not reactive with most proteins from ther spirochaetes; and/or (ii) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most to specific nucleic acid sequences but not to genomic DNA from most conserved to protect against infection by B. burgdorferi sensu lato.

(I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi sensu lato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis,
                                                                                                                                 7
responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis, compared with use of whole bacteria as antigen.
                                                                                                                                                                                                                           IGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVV 120
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                1 MNKLLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFG 60
                                                                                                                                                                                                                                                                                        TMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSALGFELSFKKSY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid from Borrelia burgdorferi encoding virulence associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorrella; P13 antigen; spirochaete; vaccine; infection; diagnosis.
                                                                                                                                 7
                                                                                                Length 177;
                                                                                                                                 Indels
                                                                                                                               18;
                                                                                                81.7%; Score 737; DB 20;
81.0%; Pred. No. 4e-76;
                                                                                                               Pred. No. 4e-76;
                                                                                                                               14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 8; Page 118; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        Ą.
                                                                                                                                                                                                                                                                                                                                                                                                   AAY04282 standard; Protein; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0059036.
97DK-0001041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-IB01424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                              Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pl1 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-215027/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SYMB-) SYMBICOM AB
                                                                                                               Similarity
                                                                177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX30115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09912960-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bergstroem S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P13
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY04282;
                                                                Sequence
                                                                                                Query Match
                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                       AAY 04 282
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                                                                                                                                                                                                                                                                                                                                                                                                    SSSSXS
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The present sequence represents a Borrella burgdorferi B313 N-terminal peptide. The present invention describes an isolated nucleic acid (I) that: (I) encodes a polypeptide fragment (II) immunologically reactive with rabbit polyclonal antibody raised against a 13 kDa polypeptide of Borrella burgdorferi B313, but not reactive with most proteins from other spirochaetes; and/or (ii) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most other spirochaetes (I), (II) and transformed cells are useful in vaccines to protect against infection by B. burgdorferi sensu lato.

(I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immnoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The I3 kD protein is involved in virulence and is highly conserved within B. burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sensu lato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide
                                                                                                                                                 1 MNKLLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFG 60
   present sequence
                                                                                                                    Gaps
                                                                                                                                                                     Nucleic acid from Borrelia burgdorferi encoding virulence associated protein P13
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia; P13 antigen; spirochaete; vaccine; infection; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a more specific and sensitive antibody response, and diagnosis, compared with use of whole bacteria as antigen.
                                                                                                                    ب
ب
                                                                                 Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 25;
compared with use of whole bacteria as antigen. The prese represents a pl1 protein sequence from a best hit search
                                                                                                                  Indels
                                                                                DB 20;
                                                                                ; Score 155.5; DB 20;
; Pred. No. 6.1e-10;
12; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi B313 N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.2%; Score 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Page 49; 118pp; English.
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                                                                                                                                                                                                                 82
                                                                                                                                                                                                                               ||||| ||| :|| :|| :|| :|| IGSFVQGDYIGGGSVLGFNLLG 79
                                                                                                                                                                                                                                                                                                                           AAY04281 standard; peptide; 25
                                                                                 ch 17.2%;
1 Similarity 41.5%;
34; Conservative 1
                                                                                                                                                                                                                IGSFAQGDILGGSLILGFDAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0059036,
97DK-0001041,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-IB01424
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-215027/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYMB-) SYMBICOM AB
                                                 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bergstroem S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09912960-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                              17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1999
                                                                                                                                                                                                                                                                                                                                                               AAY04281;
                                                   Sequence
                                                                                 Query Match
Best Local
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                                                                                                              Matches
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RESULT 8

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Essential bacterial genes in Haemophilus influenzae necessary for bacterium's growth and survival, useful for screening inhibitors opolypeptides and developing therapeutic agents e.g. antimicrobial
                                                                                                                           antiparasitic agent; insecticidal agent; antibacterial agent; mucous membrane infection; otitis media; sinusitis; bronchitis; alveolitis; conjunctivitis; pneumonia; meningitis; epiglottis; cellulitis; septic arthritis.
                                                                                                    Haemophilus influenzae essential gene #24.
                                                                                                                                                                                                                                                                                                                                                                                                                       Reich KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 89; 185pp; English.
           AAU91446 standard; Protein; 378
                                                                                                                                                                                                                                                                                                                         22-AUG-2001; 2001WO-US26245
                                                                                                                                                                                                                                                                                                                                                        25-AUG-2000; 2000US-0649145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.3%;
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Best Local Similarity 28.3%
                                                                                                                                                                                                                                                                                                                                                                                                                       Chovan LE, Hessler PE,
                                                                                                                                                                                                                              Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-304258/34.
                                                                                                                                                                                                                                                                                                                                                                                        (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-304258,
N-PSDB; ABK64932
                                                                                                                                                                                                                                                           WO200218601-A2.
                                                                       18-JUN-2002
                                                                                                                                                                                                                                                                                          07-MAR-2002
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                                          AAU91446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF94145 to AAF94409 represent essential bacterial genes from Haemophilus influenzae, which encode the proteins given in AAB88492 to AAB88556. The present in also describes methods for identifying essential bacterial genes (i.e. those essential to the survival of a bacterium) using a transposition system. The methods are used to identify essential genes from bacteria, especially H. influenzae (which causes otitis media, meningitis and upper respiratory tract infections) which may be used as targets for potential antimicrobial agents.

AAF94410 to AAF94416 represent PCR primers used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Essential bacterial genes from Haemophilus influenzae and methods for identifying 'essential' genes that may be potential therapeutic targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVVTMAVTRL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 VFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPF-----LLNLFLGFGIGSFAQG 67
                                                                                                                                                                                                                                                                                        Haemophilus influenzae; essential bacterial gene; identification; otitis media; meningitis; upper respiratory tract infection; infection; antimicrobial.
                                                                                                                                                                                                                                                           Haemophilus influenzae essential bacterial protein SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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                           Indels
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                         ö
            1.4e-07;
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                         Mismatches
            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 88-89; 185pp; English
                                                                                                                                                                  AAB88515 standard; Protein; 378 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reich KA;
                                                          99
                                                                         1 TSKQDPIVPFLLNLFLGFGIGSFAQ 25
100.08; Fr. 0;
                                                        TSKQDPIVPFLLNLFLGFGIGSFAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-2000; 2000WO-US21176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0368382
                                                                                                                                                                                                                            04-JUN-2001 (first entry)
                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hessler PE,
                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-147511/15.
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es 34; Conserv
         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF94368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chovan LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                 AAB88515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                         Matches
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AAU91446
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The invention describes an essential bacterial gene (I) comprising a purified polynucleotide isolated from Haemophilus influenzae where (I) is essential to H. influenzae survival. The encoded polypeptide (II) is useful for screening substances that function to inhibit essential H. influenzae polypeptides by contacting (II) with the desired substances and measuring the response by a screen from specific, enzyme, general, affinity, phenotypic and binding screen. (I) and (II) are useful in developing therapeutic agents such as antifungal, antibacterial and antiparasitic agent, insecticidal agent, and preventive antimicrobial agents which are effective in preventing microbial infection or useful in treatment of that particular infection: (I) and (II) may also be useful in treatment of mucous membrane infections such as otitis media, aniusitis, bronchitis, alveolitis, conjunctivitis, pneumonia, meningitis, epiglottis, celiulitis and septic arthritis. This is the amino acid sequence of an essential H. influenzae gene, described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ς.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 VKSFFGLSGDGKTAIIEMAAASGLHLVPPEKRNPLLTTSYGTGELIKLALDLGVESFILG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVVTMAVTRL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --IGGS---AINDGGVGMLQA---LGMQCLDSQDKPIGF-----GRAELANIVKIDVQQL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 VFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPF-----LLNLFLGFGIGSFAQG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Score 84.5; DB 23;
28.3%; Pred. No. 0.51;
ve 19; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB93914 standard; Protein; 355 AA.
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                                                                                                                                                                                                                                                                                                                                             Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 LPIFGLKTESNFFMYVKAPAAGVILATGFVHILPDATESLTSSCLGEEPPWGDFPM-TGL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFAQGDILGGSLILGFDAVGIGLILAGAYLDI -- KALDGITKKA-AFQWTWGKGVMLAGV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 IFVLATFCVFSSFAQANDSKNGAFGMSAGEK -- LLVYETSKQDPIVPFLLNLFLG-FGIG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.3%; Score 84; DB 23; Length 355; 29.6%; Pred. No. 0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; SEQ ID NO 3125; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTMAVTRLTEIILPFTFANSY-NR----KLKNSLNVALGGFE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71;
                                           Herbicidally active polypeptide SEQ ID NO 3125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Mismatches
                                                                       Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #7102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG07111 standard; Protein; 1456 AA
                                                                                                                                                                                             28-AUG-2001; 2001WO-EP09892.
                                                                                                                                                                                                                          28-AUG-2001; 2001WO-EP09892.
               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                       Weidler M;
                                                                                                    Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful as herbicides
                                                                                                                                                                                                                                                                                                                   WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 AA;
                                                                                                                                                                                                                                                         (FARB ) BAYER AG.
                                                                                                                                  WO200210210-A2.
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                                                                                                                                                                 07-FEB-2002
                                                                                                                                                                                                                                                                                       rietjen K,
                                                                                                                                                                                                                                                                                                                                                                                             organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Matches
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PER) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and continuous and sequences of the invention.

Note: The sequence data for this patent did not appear in the printed sequence in the printed and polymeration of electronic format directly from WIPO
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21.1%; Pred. No. 3.5;
ive 32; Mismatches 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 37470; 103pp; English.
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NYNIGQIALSFSKAPDKGTEIAIE
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                                                                                                 30-MAR-2001; 2001WO-US08631
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23-AUG-2000; 2000US-0649167
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Tateishi N,
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                                                                                                                   RESULT 13
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Configuration, but was obtained in electronic format directly from WIPO specification.
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                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 54873; 103pp; English.
                                                                          Novel human diagnostic protein #24505.
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2000US-0649167
                                    18-FEB-2002 (first entry)
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ABG24514;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and maniyabide the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, coryneform bacterium, and identifying a manion acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ochiai K, Yokoi H;
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                                                                                                                                                                                                                                                                                         amino acid synthesis; vitamin; saccharide;
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la M, Ozaki A;
                                                                                                                                                                                                                   glutamicum protein fragment SEQ ID NO: 3606.
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AAG89852 standard; Protein; 384 AA
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03-AUG-2000; 2000JP-0280988.
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                                                                                                                                            (first entry)
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Senoh A, I
                                                                                                                                                                                                                                                                                                                   organic acid synthesis.
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                                                                                                                                                                                                                                                                                     Coryneform bacterium;
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specification,
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14-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF70984 to AAF71133 encode the Corynebacterium glutamicum stress, resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020. The C. glutamicum SRT genes (I) can be used in vectors (II) for expression in host cells and production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated are or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine chemical production can be modulated. The presence of (I) or the SRT proteins (III) encoded by them are used for diagnosing the presence
                                                                                                                                                                                                                              Corynebacterium glutamicum; stress; resistance; tolerance; SRT; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrinidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; evolutionary study; environmental hazard; fermentation.
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                                -----GLVVSAGTAWAGRLRGASGVTLAGIILTAGFWMGPIVTSGLGMASTSIITPFA 163
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                                                       FANSYNRKLKNSLNVALGGF-----EPSFDVAMGQSSALGFELSFKKS 178
                                                                      C. glutamicum SRT protein sequence SEQ ID NO:162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schroeder H, Zelder O,
        92 LDIKALDGITKKAAFQWT----WGKGVMLAGVVTMA---
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                                                                                                                                      AAB78951 standard; Protein; 384 AA
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99US-0151214.
99DE-1041382.
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99US-0142692.
99DE-1031413.
99DE-1031457.
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99DE-1032914.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carbohydrates, or enzymes -
                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum.
                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-061972/07.
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27-AUG-1999;
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                                                                                                                                                             AAB78951;
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                                                      136
                                                                                                               RESULT 14
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cells containing them can be used to map the genomes of organisms related to C. glutamicum, to identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determination of SRT protein aregions required for function, in modulating the SRT protein activity, and in modulating the SRT protein activity, and in modulating the SRT protein activity, end in modulating the SRT protein activity, end in modulating the SRT protein activity, end in modulating the srr pathway. (II) are used to permit C. glutamicum to survive in a environment that is normally environmentally or chemically hazardous to it. (I) and protein molecules encoded by it increase the survival of C. glutamicum to chemical and multiplication in large scale fermentative growth conditions. By increasing the growth rate or maintaining a normal growth rate in poor or toxic conditions, the yield, production and/or efficiency or production of fine chemicals from a culture may be increased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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activity of Corynebacterium diphtheriae. (I), (II), (III) and host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 LDIKALDGITKKAAFQWT----WGKGVMLAGVVTMA-----VT-----RLTEIILPFT 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GEKLLVYETSKQDPIVPFLLNLFLGFGIGSFAQGDILGGGSLILGFDAVGIGLILAGAY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 FANSYNRKLKNSLNVALGGF-----EPSFDVAMGOSSALGFELSFKKS 178
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24.3%; Pred. No. 0.68;
ive 24; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB78952 standard; Protein; 369 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 AA;
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Best Local 3
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AAF70984 to AAF71133 encode the Corynebacterium glutamicum stress, resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020.

The C. glutamicum SRT genes (I C) can be used in vectors (II) for carbor calls and production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic anino acid (preferred), a purine or pytimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine corporate production can be madulated. The presence of (I) or the SRT proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae. (I), (III) and host colls containing them can be used to map the genomes of organisms related to c. glutamicum, to identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determination of SRT protein and in modulating the activity of an SRT pathway. (II) are used to permit cequions required for function, in modulating the SRT protein molecules and in modulating the activity of an SRT pathway. (II) are used to permit continuementally are chemically hazardous to it. (I) and protein molecules encoded by it increase the survival of C. glutamicum to chemical and environmental hazards and provide a means for continued growth and environmental hazards and provide a means for continued growth and continued growth rate or maintaining a normal growth rate in poor or toxic conditions, the yield, production and/or efficiency or production and continued stream conditions are conditioned growth and continued growth rate in poor or toxic orditions the yield or maintaining a normal growth rate in poor or continued proverses.
                                                                                                                                             Lee H;
                                                                                                                                                                                                                                                                                                             New isolated Corynebacterium glutamicum nucleic acid encoding a stress, tolerance or resistance protein, for production or modulation of production of fine chemicals, such as, e.g. amino acids, lipids,
                                                                                                                                          Schroeder H, Zelder O, Haberhauer G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 327-328; 526pp; English.
99US-0151214.
99DE-1041382.
                                                                                                                                                                                                                                                                                                                                                                                               carbohydrates, or enzymes
                                                                                                                                          Pompejus M, Kroeger B,
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27-AUG-1999;
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74; Gaps Match 9.1%; Score 82; DB 22; Length 369; Local Similarity 26.4%; Pred. No. 0.95; les 51; Conservative 19; Mismatches 49; Indels Query Match Matches

11;

-----VT-----EPSFDVAMGQ 165 69 ILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWT----WGKGVMLAGVVTMA- 123 81 --GPSLLVGRFIVGLGV------GLVVSAGTAWAGRLRGASGVTLAGIILTAG 125 126 FWMGPIVTSGLGMASTSIITPFAIS-----VALSLIAVVVGFALGDARSTPS---ALGA 176 NGAFGMSA------GEKLLVYETSKQDPIVPFLLNLFLGFGIGSFAQGD 68 31 NGAFGIYALGLLPSLLAGGVLADRFGARMVVLTGG----VLSALGNLSL-----LAFHD 80 56 124 g ò g q ò ò

166 SSALGFELSFKKS 178

SSGIKHERSMKKA 189

Search completed: March 14, 2003, 14:24:22 Job time: 33.1742 secs

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1 5.1.4_p5_4578 Compugen Ltd. GenCore version Copyright (c) 1993 - 2003

- protein search, using sw model OM protein March 14, 2003, 14:22:16 ; Search time 12.4026 Seconds
 (without alignments)
 1387.454 Million cell updates/sec Run on:

US-09-508-487-19

1 MNKLLIFVLATFCVFSSFAQ......DVAMGQSSALGFELSFKKSY 179 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

inimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

PIR_73:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	conserved hypothet		conserved hypothet		hypothetical prote		hypothetical prote	ø	C4-dicarboxylate t	sodium-glutamate s	hypothetical prote	Na+/H+ antiporter	conserved hypothet	undecapreny1-phosp	hypothetical prote	flagellar protein	NADH2 dehydrogenas	cytochrome d ubiqu	probable transmemb	hypothetical prote	probable phosphate	C4-dicarboxylate t	C4-dicarboxylate t	PTS system, fructo	phosphotransferase	oligopeptide trans	comE protein - Syn	hypothetical prote
	er e	B70104	A70207	F70243	G70239	G98325	AG2957	537867	S76538	T44611	AI0485	н69822	S61393	F83814	C64142	H70346	T34251	JC4509	T11491	875272	T35791	C33958	D81325	C96032	A33597	C95101	D97969	A87577	S75212	S73384
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hypothetical prote	metabolite export hypothetical prote	conserved hypothet	phosphate transpor	amidophosphoribosy	glycogen phosphory	cellulose 1,4-beta	alcohol dehydrogen	alcohol dehydrogen	phosphoglucomutase	probable dctA prot	probable CDP-alcoh	conserved hypothet	conserved hypothet	PTS system, galact
G71246	A41901 C97662	AF2886	AC0956	S77612	H70362	S59077	AH2781	н97560	C72408	A70681	E71157	E89938	T38152	АН0898
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385	938 866	998	319	493	692	1090	375	375	429	491	188	235	240	457
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80	08	80	79.5	79.5	79.5	79	78.5	78.5	78.5	78.5	78	78	78	78
30	37 32	33	34	35	36	37	38	39	40	41	42	43	44	45

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hypothetical protein BB0034 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: B70104
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; W
Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; W
Suture 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; WUID: 98065943; PMID: 9403685
A;Accession: B70104
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-179 <KLE>
A;Cross-references: GBAEC01117; GB:AE000783; NID: 92687907; PIDN: AAC66426.1; PID: 926
A;Cross-references: GBAEC01117; GB:AE000783; NID: 92687907; PIDN: AAC66426.1; PID: 926
A;Cross-references: GB:AEC01117; GB:AE000783; NID: 92687907; PIDN: AAC66426.1; PID: 926
A;Cross-references: GB:AEC01117; GB:AE000783; NID: 92687907; PIDN: AAC66426.1; PID: 926
A;Cross-references: GB:AEC01117; GB:AE000783; NID: 92687907; PIDN: AAC66426.1; PID: 926
A;Cross-references: GB:AEC01117; GB:AE000783; NID: 92687907; PIDN: AAC66426.1; PID: 9268
A;Cross-references: GB:AEC01117; GB:AE000783; NID: 92687907; PIDN: ACC6426.1; PID: 92687907; PIDN: ACC6426.1; PID: 92687907; PID: 92

ö 0; Gaps Length 179; Indels Query Match 100.0%; Score 902; DB 2; Best Local Similarity 100.0%; Pred. No. 3.5e-73; Matches 179; Conservative 0; Mismatches 0;

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61 IGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVV 120 g δ

TMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSALGFELSFKKSY 179 121 οy

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RESULT 2

Conserved hypothetical protein BBA01 - Lyme disease spirochete plasmid A/lp54 C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 17-Mar-2000
C; Accession: A7027
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, I Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Authors: Smith, H.O.; Venter, J.C.
A; Attle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID:98065943; PMID:9403685

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A; Accession: A70207

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conserved hypothetical protein BBI31 - Lyme disease spirochete plasmid 1/lp28-4 C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 17-Mar-2000
C; Accession: F70243
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White Son, D.; Feterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. A; Authors: Smith, H.O.; Venter, J.C.
A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID:98065943; PMID:9403685
                                                                A;Cross-references: GB:AE000790; NID:g2690224; PIDN:AAC66226.1; PID:g2690225; TIGR:BBA01
A;Experimental source: strain B31
C;Genetics
A;Genome: plasmid
C;Superfamily: Lyme disease spirochete plasmid hypothetical protein BBA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:AE000789; NID:92690079; PIDN:AAC66194.1; PID:92690091; TIGR:BB131
                                                                                                                                                                                                                                                                        8
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G70239
Conserved hypothetical protein BBH41 - Lyme disease spirochete plasmid H/lp28-3
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                        64 FAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGV----- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---MLAGV-VTMAVTRLT-EIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSAL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFGIGS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNKLLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 MKKILTLILIFSLTIQIFATQDKLEK ---SVGSIETIMKYKSEKATILAPFLLNLFLTLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSALGFELSFKKSY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: Lyme disease spirochete plasmid hypothetical protein BBA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 170;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                  32.3%; Score 291; DB 2; L 39.5%; Pred. No. 7.9e-19; attive 23; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 31.0%; Score 279.5; DB 2; Best Local Similarity 36.9%; Pred. No. 8.8e-18; Matches 66; Conservative 29; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Experimental source: strain B31
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFELSFKKSY 179
                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 GFQLSFKKSY 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA Residues: 1-170 < KLE>
                                      1-161 <KLE>
                    A;Molecule type: DNA
A;Residues: 1-161 <K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115
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A;Cross-references: GB:AE000784; NID:g2690041; PIDN:AAC65989.1; PID:g2690045; TIGR:BB
A;Experimental source: strain B31
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 17-Mar-2000
C;Accession: G70239
R;Fraser, C.M.; Casjens, S.; Hang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Attle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Attle: Groomic G70239
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-190 <KLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 ALDGITKKAAFQWTWGKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 OMKNLKKEPAS--ISSMILLLSGMLTFGSSYLISIYLPVLFEDRYYKNLMNRIIDELAGF 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| :| : | : | : | : | 360 LILATATNLSVGSLLVGGFFAGGLM----AVCLGVAI---HLSVRSVDTLPRATGAERWR 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TWGKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
A; Genome: plasmid
C; Superfamily: Lyme disease spirochete plasmid hypothetical protein BBA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 LLVYETSKQ-DPIVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LATFCVFSSFAQANDSKNGAFGMSAGEKLLVYE-----TSKQDPIVP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.1%; Score 235; DB 2; Length 190
Best Local Similarity 38.9%; Pred. No. 9e-14;
Matches 56; Conservative 25; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 EPSFDVAMGQSSALGFELSFKKSY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 EPNLDIGMN-----GFQLSFKKSY 190
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Best Local Similarity 22.29
Matches 42; Conservative
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Mon Mar 17 12:24:36 2003

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16; Gaps

Indels

39;

DB 2; Length 449;

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C.Species: Synechocystis sp.
A; Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S76538
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Ya DNA Res. 3, 109-136, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytochrome caa3 oxidase assembly factor [imported] - Bacillus cereus
C;Species: Bacillus cereus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T44611
R;Okstad, O.A.; Hegna, I.; Lindbaeck, T.; Rishovd, A.L.; Kolsto, A.B.
Microbiology 145, 621-631, 1999
A;Title: Genome organisation is not conserved between Bacillus cereus and Bacillus s A;Reference number: Z22811; MUID:99231848; PMID:10217496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 VGIGLILAGAYL----DIKALDGITKKAAFQWTWGKGVMLAGVVTMAVTRLTEIILPFTF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 VPFLLNLFLGFGIGSFAQGDIL------GGSLILGFDAVGIGLILAGAYLDIKA 96
                            A;Cross-references: EMBL:X71621
A;Experimental source: strain $288C
A;Experimental source: strain $288C
G;Genetics:
A;Cross-references: SGD:S0001529
A;Map position: 11L
C;Superfamily: Schizosecharomyces pombe hypothetical protein SPCC970.02
C;Reywords: transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>F;23-449/Product: hypothetical protein YKL046c #status predicted <MMT>
F;431-447/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 86; DB 2; Length 214;
Pred. No. 1.9;
9; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 VGVNLISNGTYKYVYDGVSIDDNCTKVTSYQWTYNQGLLLAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein – Synechocystis sp. (strain PCC 6803)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 ANSYNRKLKNSLNVALGGFEPS--FDVA-MGQSSALGFELSFK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Reference number: S74322; MUID:97061201; PMID:8905231
A, Accession: S76538
A, Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.6%; Score 87; DB 2 Best Local Similarity 27.2%; Pred. No. 3.3; Matches 28; Conservative 20; Mismatches
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Local Similarity 31.3%;
les 31; Conservative
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A; Residues: 1-214 <KAN>
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A; Residues: 1-307 <OKS>
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Matches
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                                                                                                                                                                                                                                                               hypothetical protein Atu3261 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) (Species: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens (C59ecies: Agrobacterium tumefaciens (C50ecies: Agrobacterium tumefaciens) (C50ecies: Agrobacterium tumefacies: Agrobac
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R.Purnelle, B. Tettellin, H.; van Dyck, L.; Skala, J.; Goffeau, A.
Yeast 9, 1379-1384, 1993
A.Title: The sequence of a 17.5 kb DNA fragment on the left arm of yeast chromosome XI is even new open reading frames.
A.Reference number: $40650; MUID:94205268; PMID:8154189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ster, E.W.

A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A.Reference number: AB2577; PMID:11743193

A.Recession: AG2957

A.Status: preliminary

A.Molecule type: DNA

A.Kesidues: 1-616 < KURN>
A.Kerss-references: GB:AE008689; PIDN:AAL44077.1; PID:g17741642; GSPDB:GN00187

C.Genetics:

C.Genetics:
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hypothetical protein YKL046c precursor - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YKL259
C:Species: Saccharomyces cerevisiae
C:Species: May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002
C:Accession: S37867; S40654
R:Purnelle, B.; Skala, J.; van Dyck, L.; Tettelin, H.; Goffeau, A.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S37851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 SAIAAIPAFGLGVIVVVGIRIGIVTTTEAA---ALAALYTLLIGFGYRLGVGRIFATFRQ 469
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162 AMGQSSALG 170
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470 SAGEAAAIG 478
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C4-dicarboxylate transport protein dctA [imported] - Yersinia pestis (strain CO92)
C5.Specias: Yersinia pestis
C5.Specias: Yersinia pestis
C5.Date: 02-Nov-2001
C5.Accession: A10485
R5.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R7.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
A7.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A7.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A7.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A7.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A7.Title: Genome sequence of Yersinia pestis, The Causative agent of plague.
A7.Title: Genome sequence of Yersinia pestis, The Causative agent of plague.
A7.Title: Genome sequence of Yersinia pestis, The Causative agent of plague.
A7.Title: Genome sequence of Yersinia pestis, The Causative agent of plague.
A7.Title: Genome sequence of Yersinia pestis, The Causative agent of Plague.
A7.Title: Genome sequence of Yersinia pestis, The Causative agent of Plague.
A7.Title: Genome sequence of Yersinia pestis, The Causative agent of Plague.
A7.Title: Genome sequence of Yersinia pestis, The Causative agent of Plague.
A7.Title: Genome sequence of Yersinia pestis, The Causative agent of Plague.
A7.Title: Genome sequence of Yersinia pestis, The Causative agent of Plague.
A7.Title: Genome sequence of Yersinia pestis, The Causative agent of Plague.
A7.Title: Genome sequence of Yersinia pestis, The Causative agent of Plague.
A7.Title: Genome Sequence of Yersinia pestis, The Causative agent of Plague.
A7.Title: Genome Sequence of Yersinia pestis, The Causative agent of Plague.
A7.Title: Genome Sequence of Yersinia pestis and The Causative agent of Plague.
A7.Title: Genome Sequence of Yersinia pestis and The Causative agent of Plague.
A7.Title: Genome Sequence of Yersinia pestis and The Causative A7.Title: Genome Sequence of Yersinia pestis and The Causative A7.Tit
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: H69822
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
                                                                                                                                                                                                                                                                                                                                                                                                          7;
A;Cross-references: EMBL:AJ010111; NID:94584147; PIDN:CAB40606.1; PID:94584150 A;Experimental source: AFCC 10987 C;Genetics: Asonce: ctaB C;Superfamily: heme O synthase
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                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                           Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                 58; Indels
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Pred. No.
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Best Local Similarity 25.0%; Pre
Matches 49; Conservative 30;
                                                                                                                                                                                                                                                                                                                                                                         38; Conservative
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250 FKFIRYIKEELLIVLG 265
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A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari Nature 390, 249-256, 1997

A;Authors: Foundger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; G iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardil, A;Authors: Lauber, J.; Lazarevic, V.; Face, S.M.; Levine, A.; Liu, H.; Masuda, S.; M.; M.; Muthors: Lauber, J.; Lazarevic, V.; Park, S.H.; Parro, V.; Pohl, T.M.; Porte, R.; Schleich, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rask, M.; Sadaie, Y.; Sato, T.; Scal A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; E akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tanaka, T.; Tanamanoto, H.; Zumatein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiy, A.; Wilpet, A.; Yamamoto, H.; Yamano, K.; Yasumoto, K.; Yata, K.; Yoshi, A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtill A;Reference number: A69580; MuID:98044033; PMID:9384377

A;Residues: 1-463 <KUN>
A;Residues: 1-463 <KUN>
A;Residues: 1-463 <KUN>
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C;Species: Bacillus sp.
A;Variety: Strain C-125
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 15-Oct-1999
C;Accession: S61393
R;Hamamoto, T.; Hashimoto, M.; Hino, M.; Kitada, M.; Seto, Y.; Kudo, T.; Horlkoshi, . Mol. Microbiol, 14, 939-946, 1994
A;Title: Characterization of a gene responsible for the Na(+)/H(+) antiporter system A;Reference number: S61392; MulD:95231300; PMID:7715455
A;Accession: S61393
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA
A;Residues: 1-146 <HAM>A;Residues: 1-146 <HAM>A;Residues: 1-146 <HAM>A;Residues: I-146 <HA
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C; Accession: H70346
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A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05037.1; GSPDB:GN00
A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05037.1; GSPDB:GN00
A;Sperimental source: strain C-125
C;Genetics:
A;Gene: BH1318
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Cypecession: C54142
Cypecies: Haemophilus influenzae
Cypecession: Cypecies:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1.378 <TIGR>
A; Cross-references: GB:U32694; GB:L42023; NID:g1573035; PIDN:AAC21769.1; PID:g1573042; C; Superfamily: yhaD protein
                                                                                                                                             C.Accession: F83814
R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; I Nucleic Acids Res. 28, 4317-4331, 2000
A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A.Reference number: A83650; MUID:20512582; PMID:11058132
A.Accession: F83814
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-146 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         undecaprenyl-phosphate-alpha-N- acetylglucosaminyltransferase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٠,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein H10091 - Haemophilus influenzae (strain Rd KW20)
                                                                         C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 VKSFFGLSGDGKTAIIEMAAASGLHLVPPEKRNPLLTTSYGTGELIKLALDLGVESFILG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --IGGS---ATNDGGVGMLQA---LGMQCLDSQDKPIGF-----GGAELANIVKIDVQQL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVVTMAVTRL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNKLLIFVLATFCVFSSFAQANDSKNGAFG--MSAGEKLLVYETSKQDPI---VPF---- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 -----LLNLFLGFGIGSFAQGD------ILGGSLI---LGFDAVGIGLILAG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 VFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPF-----LLNLFLGFGIGSFAQG 67
                                  BH1318 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 378;
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A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.4%; Score 85; DB 2;
28.8%; Pred. No. 1.6;
ative 19; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Conservative
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Best Local Similarity
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Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 AYLDI 94
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H70346
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14 VFSSFAQANDSK-----NGAFGMSAGEKLLV----YETSKQDPIVPFLLNLF----LG
                                                                                                                                                                                           9.3%; Score 84; DB 2; Length 357;
llarity 32.3%; Pred. No. 4.8;
Conservative 15; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                            199 FFLWNYPFGLIFLGDGGAYFLGFCAGAIGAILVNKYPDI 237
                                                                                                                                                                                                                                                                                                  59 FGIGSFAQGDIL---GGSLILGFDAVGIGLILAGAYLDI
                                                                                                                                                                                                                                                                                                                                                                Search completed: March 14, 2003, 14:25:39 Job time: 15.4026 secs
                                                                                                                                                                                                       Local Similarity
es 32; Conserv
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us-09-508-487-19.rsp

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2003, 14:21:36 ; Search time 7.37453 Seconds
 (without alignments)
 1006.744 Million cell updates/sec Run on:

US-09-508-487-19 902 1 MNKLLIFVLATFCVFSSFAQ......DVAMGQSSALGFELSFKKSY 179 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

inimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMARIES		
Result		Query					
. No. :	Score	Match	Length	DB :	a	Description	ption
1	87	•	449	-	YKE6_YEAST	P36091	saccharomyc
7	8	•	429	Н	DCTA_YERPE	08za28	yersinia pe
m	'n.		463	Н	YHCL_BACSU	P54596	bacillus
4	84.5	4.6	378	Н	GRK_HAEIN	P44507	haemophil
'n	ď	•	265	-	FLIR_TREPA	P74932	
9	ä	•	174	٦	NU6M_RABIT	079438	oryctolagu
7	α	•	461	-	PUCC_RHOCA	P23462	
œ	80.5	•	441	Н	DCTA_RHIME	P20672	
6	ö	•	497	Н	DCTA_RHISN	P31601	
10	80	٠	264	Н	YA96_MYCPN	P75596	
11	œ	٠	538	Н	TCMA_STRGA	P39886	
12	79.5	•	493	Н	PUR1_SYNP7	055038	
13	σ.	•	692	Н	PHSG_AQUAE	066932	
14	79	•	1090	Н	GUXB_CELFI	P50899	
15	78	•	188	 1	Y460_PYRHO	058215	pyrococcus
16	7	•	576	Н	MOES_PIG	P26042	
17	77.5	•	151	П	YQ00_MYCPA	Q9k537	
18	7	٠	310	П	YQEW_BACSU	P54463	
19			371	7	OOXB_AGRT4	059159	
20	76.5		380	-	OPS4_DROPS	P29404	
21		•	534	Н.	HUP3_CHLKE	039525	
22	7	•	534		HUP1_CHLKE	P15686	
23	5.		356	٦	YUXJ_BACSU	P40760	bacillus su
24	75.5	•	845	Н	CC47_YEAST	P38132	saccharomyc
25	5		989	7	SMB2_MESAU	095090	mesocricetu
26		•	263		LPXA_CAMJE	Q9pim1	campylobact
27		٠	347	-	RNHL_DROME	09vpp5	drosophila
28			447	Н	Y418_HAEIN	P44699	haemophilus
29			576	Н	MOES_HUMAN	P26038	homo sapien
30			576	-	MOES_MOUSE	P26041	mus musculu
31	75		595	-	HMD2_SOLTU	33	solanum tub
32	_		099	Н	CCMF_BRAJA	P45403	bradyrhizob
33	74.5	•	197	-	NORE_NEIMA	Q9jvq2	neisseria m

8 11 5

81 VGIGLILAGAYL----DIKALDGITKKAAFQWTWGKGVMLAGVVTMAVTRLTEIILPFTF 136

137 ANSYNRKLKNSLNVALGGFEPS--FDVA-MGQSSALGFELSFK 176 SDLWHTRTKEFLNASQVFFHDGIVYEAACQGPNSCNTDQRSFK 311

269

Qy Dp

ΩD

P39381 escherichia Q8678 rhizoblum 1 Q12556 aspergillus P21652 arabidopsis P1764 drosophila P4331 escherichia Q9k0m7 nelsseria m Q91475 pseudomonas Q0187 rhizoblum 1 Q9z1u5 bacillus th Q55886 synechocyst P37189 escherichia		DB 1; Length 449; ; es 39; Indels 16; Gaps 4;
J ECOLI 2_RHILO 1_RARNG R_ARATH 4_DROVI M_E_NEIMB A_PSEAE A_RHILE B_BACTV Y_SYNY3 C_ECOLI	update) update) update) on update M1-PRI2 east). aromycot ae; Sacc ae; Sacc ing a pu informat te. The s long te. The coved iAL. iAL. iAL.	ore 87; DB ed. No. 2; Mismatches
YJIJ_ECOLI DTAZ_RHID AMO1_ASPNI TIPR_ARATH OPS4_DROVI YNFM_ECOLI NORE_NEIMB DCTA_PERAE DCTA_RILE CBBB_BACTY MRAY_SYNY3 PTKC_ECOLI	STANDARD; PRT; 449 AA. (Rel. 29, Created) (8el. 35, Last sequence update) (8el. 35, Last sequence update) (8el. 35, Last annotation update) (8el. 35, Last annotation update) (8el. 35, Last annotation update) (8el. 35, Last annotation update) (8el. 35, Last annotation update) (8el. 35, Last annotation update) (8el. 35, Last annotation update) (8el. 1093; (8el. 17.5 kb DNA fragment on the profice of a 17.5 kb DNA fragment on the profice of a 17.5 kb DNA fragment on the profice of a 184 (1993). (1384 (1993). (17. TO YEAST WR238W. (184 (1993). (184 (1993). (184 (1993). (185 DNA FRAGARD OF ENOTINE OF ENOTERITAL. 10 PROFINE TRANSMEMBRIANE. 10 PROFINE OF ENOTERITAL. 11 PROFINE OF ENOTERITAL. 12 PROFINE OF ENOTERITAL. 13 PROFINE OF ENOTERITAL. 14 PAA, 49565 WW; DECEPSORFEDSSY	Score 87; Pred. No.
YJIJ DJAZJ DJAZJ AMOJ TJPR OPSK YNEM NORE DCTA DCTA MRAY PTKC	seed) seed)	20
ненененен	ARD; Created) Last sequence of the protein a	9.6%; 27.2%; ive
392 4422 2071 2071 1197 4436 456 456 456 456	STANDARD; Rel. 29, Created) Rel. 29, Last seqquel. 29, Last annowance. Sel. 35, Last annowance. Sel. 35, Last annowance. Serevisiae (Bakeronyorgi, Ascomyocta; Saccharomyocta; Saccharomyocha	9. larity 27. Conservative
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	STAND 994 (Rel. 29 994 (Rel. 29 997 (Rel. 29 997 (Rel. 35 97 (Re	lar
444 444 7.444 7.574 444 7.574	T. 1 YEAST YEAST YEAST YEAST YEAG. TEANDARD; PRT; 449 AA. 19566; While the control of the contr	Query Match Best Local Similarity Matches 28; Conser
4 5 5 5 6 5 6 6 7 7 8 8 8 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9	RESULT 1 ID FREE TYRE TYRE TYRE TYRE TYRE TYRE TYRE T	Query M Best Lo Matches
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YHCL_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                        Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).

I FUNCTION: Responsible for the transport of dicarboxylates such as succinate, fumarate, and malate from the periplasm across the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 GITKKAAFQWTWGK-GVMLAGVVTMAVTRLTEIILPF------TFA--NSYN- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 IPGSVVGAFASGNILQVLLFAVLFGFALHRLGEKGQLIFNVIESFSRVIFGVINMIMRLA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54; Gaps
                                                                                                                                                                                                                                                                                                                                                                    (By similarity).
SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LLIF-VLATFCVFSSFAQANDSKNGAFGMS-----AGEKLLVYETSKQDPIVPFLLNL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLGFGIGSFAQGDILG---GSLILGFDAVGIG------LILAGAYLDIKALD 98
                                                                                                                                                                                                                                                                                                                                           membrane (By similarity).
SUBCELLUIAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00713; NA_DICARBOXYL_SYMP_1; 1.
PROSITE; PS00714; NA_DICARBOXYL_SYMP_2; 1.
Transport; Sugar transport; Transmembrane; Inner membrane; Symport;
Complete proteome.
                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
29454320410770C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
                                                           15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                          429 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.5%; Score 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                   C4-dicarboxylate transport protein. DCTA OR YPO3992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001991; Na/dico_symp. 
Pfam; PF00375; SDF; 1.
                                                                                                                                                                                    STRAIN-CO-92 / Biovar Orientalis;
MEDLINE-21470413; PubMed=11586360;
                                                15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45498 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ414160; CAC93453.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                             (SDF, TC 2.A.23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330
351
429 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                             Versinia pestis
                                                                                                                                                NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                      DCTA_YERPE
Q8ZA28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
TRANSMEM
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Matches 4
RESULT 2
DCTA_YERPE
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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Brischi C.V., Connerton I.F., Cummings N.J., Daniel R.A.,

Rhois.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galieron N.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Mustra K., Lapidus A., Lardhois S., Lauber J., Lazarevic V.,

RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott R.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

Sekiguchi J., Sekwaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Takeuchi M., Tanakoshi A., Tarkafarshi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Tarkafar T., Takahashi H., Takemaru K.,

RA Takati A., Wanbutt R., Wedler E., Wedler H., Weitzenegger T.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

RA Tosato V., Wanbutt R., Wedler E., Wedler H., Weitzenegger T.,

RA Tosato V., Wanbutt R., Wandler E., Wedler H., Weitzenegger T.,

RA Tosato W., Wanbutt R., Wandler E., Wedler H., Weitzenegger T.,

RA Toshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

Rhitis F. Philis F., Rhitis R.,

Rhitis R., Rhitis R., Rhitis R., Rhitis R.,

Rhitis R., Rhitis R., Rhitis R., Rhitis R.,

Rhitis R., Rhitis R., Rhitis R.,

Rhitis R., Rhitis R., Rhitis R.,

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    ---GSLVQLGQLILCFYLTCILFVVLVLGTIAKFNGFNI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S., "A 22 kb DNA sequence in the cspB-glpPFKD region at 75 degrees on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97124185; PubMed=8969498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtillis chromosome.";
Microbiology 142:3021-3026(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical symporter yhcL.
: | :| || || 11 || 197 PLGAFGAMAFTIGKYGV----
                                                                                                                                                                                                                                     250 FKFIRYIKEELLIVLG 265
                                                                                                                                           ----RKLKNSLNVALG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SDF, TC 2.A.23)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996
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and for commercial

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Usage by
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Flagellar biosynthetic protein fliR.
  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                       Matches 34; Conservative 19; Mismatches
                          or send an email to license@isb-sib.ch)
               entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           flip, flio, fliR and flhB' genes.";
Gene 166:57-64(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96105201; PubMed-8529894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98332770; PubMed-9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U36839; AAB00548.1; -.
                                                                                                                                                                           28.3%;
                                                  EMBL; U32694; AAC21769.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                               HI0091
                                                                                                                                                                                                                                                                                                                                                       FLIR_TREPA
P74932;
                                                                                                                                                                Query Match
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FLIR_TREPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                  334 GSFGLSIGQNGCAGIYPAMLAMMIAPTVGQNPFDPVFIITVIAVVAISSFGVAGVGGGAT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIRAIN=Rd / KW20 / ATCC 51907;

MEDLINE-9535030; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,

Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Wenter J.C.,
                                                                                                                                                                                                                                                                                                                                          GAFGMSAGEK------LLVYETSKQDPIVP-FLLNLFLGFGIGSFAQGDILGG-- 72
                EMBL; X96983; CAA65696.1; -.
EMBL; Z99108; CAB1Z741.1; -.
Subtilist; BG11590; yhct.
Interpro; IPR001991; Na/diCO_symp.
Pfam; PF00375; SDF; 1.
PROSITE; PS00713; NA_DICARBOXYL_SYMP_1; FALSE_NEG.
PROSITE; PS00714; NA_DICARBOXYL_SYMP_2; FALSE_NEG.
HYPOCHETical protein; Transmembrane; Transport; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: ATP + (R)-glycerate = ADP + 3-phospho-(R)-
                                                                                                                                                                                                                                                                                                                                                                                           73 -SLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVVTMAVTR 126
                                                                                                                                                                                                                                                                                                                                                                                                          394 FAALLVLSSLNMPVALAGLLISIEPLIDMGRTALNV----SGSMTSGLITSKVTK 444
                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                          Length 463;
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE GLYCERATE KINASE FAMILY.
                                                                                                                                                                                                                                                                FA69EEAF5EC45F89 CRC64;
                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Glycerate kinase (EC 2.7.1.31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 AA.
                                                                                                                                                                                                                                                                                        Score 85.5; DI
Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                  Mismatches
 send an email to license@isb-sib.ch).
                                                                                                                                                                         POTENTIAL.
POTENTIAL.
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01-NOV-1995 (Rel. 32, Last seq
                                                                                                                                                                                                                                                               48982 MW;
                                                                                                                                                                                                                                                                                         9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                            125
204
245
282
304
389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLXK OR HI009]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRK_HAEIN
P44507;
                                                                                                                                                                                                                                                TRANSMEM
SEQUENCE
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GRK_HAEIN
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InterPro; IPR003747; Glycerate_kinase.
Pfam; PF02595; DUF168; 1.
TIGRFAMS; TIGR0045; Cons_hypoth45; 1.
Transferase; Kinase; Complete proteome.
SEQUENCE 378 AA; 39758 MW; EBC57937BD8838A9 CRC64; Treponema pallidum. Bacteria: Spirochaetales; Spirochaetaceae; Treponema.

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                                                                                                                                                                                                                                                                                        YLDIKALDGITKKAAFQWT-WGKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLN 149
                                                                                                                                                                                                                                                                                                                                                                                                                      197 LLLIHVSMGLLTKAAPQMNLLSEGLPLTIVVTFV---LLSVILPY------MINLFVS 245
                                                                                                                                                                                                                                                                                                                                                            137 VFLQIKGFQILFLGGVLRSFQAVNCFVFLRKQEALLLFFTKALSALFLHAMTIALPIMGA 196
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                  5 LIFVLATF --- CVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQ--DPIVPFLLN---- 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Giss1 C., Gullberg A., Arnason U.;
"The complete mitochondrial DNA sequence of the rabbit, Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                             DB 1; Length 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 174;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 174 AA; 18728 MW; 18740BB6661D09E1 CRC64;
                                                                                                                                                                               A9BFA16FEE365C09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last Sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase Chain 6 (EC 1.6.5.3).
                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 AA.
                                                                         Flagella; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                        27; Mismatches
                                                                                                                                                                                                             9.1%; Score 82.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 81.5;
                                                                                                      POTENTIAL.
                                                                                        POTENTIAL.
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                                                                                                                                                  POTENTIAL.
                                                                                                                                     POTENTIAL
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                                                                                                                                                                                                                              Pred.
                          Interpro; IPR002010; Bac_export_1.
Pfam; PF01311; Bac_export_1; 1.
PRINTS; PR00953; TYPE31MRPROT.
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InterPro; IPR001457; Oxidored_q3.
Pfam: PF00499; oxidored_q3; 1.
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 EMBL; AE001244; AAC65682.1; -.
                                                                                                                                                                              29313 MW;
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                                                                                                                                                                               265 AA;
                                                                                                                                                                                                                         Best Local Similarity
Matches 48; Conserv
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SEQUENCE FROM N.A.
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                  9
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LeBlanc H.N., Beatty J.T.;
"Topological analysis of the Rhodobacter capsulatus Pucc protein and effects of C-terminal deletions on light-harvesting complex II.";
J. Bacteriol. 178:4801-4806(1996).
-!- FUNCTION: PUCC IS REQUIRED FOR HIGH-LEVEL TRANSCRIPTION OF THE
                   Gaps
                                                 ----GIGSFAQGDILGGSLILGFDAVGIGLILAGAYL-D 93
                                                                             4 VVFLLSVMFVMGFVGFSSKPSPIYGGLGLIVSGGV-GCGIVLSFGGSFLGLMMFLIYLGG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                             Tichy H.V., Oberle B., Stiehle H., Schiltz E., Drews G.; "Genes downstream from pucB and pucA are essential for formation of the B800-850 complex of Rhodobacter capsulatus."; J. Bacteriol. 171:4914-4922(1989).
                                                                                                                                MEDLINE-92007739; PubMed-1717257;
Tachy H.V., Albien K.-U., Gad'on N., Drews G.;
"Analysis of the Rhodobacter capsulatus puc operon: the pucc gene
plays a central role in the regulation of LHII (B800-850 complex)
                                                                                                            94 IKALDGITKKAA---FQWTWGKGVMLAG------VVTMAVTRLTEIILPF 134
                31;
                                                                                                                                                                                                                                                                                                                                     Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                35; Indels
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
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Last annotation update)
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 Pred. No. 2.4;
                18; Mismatches
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01-NOV-1991 (Rel. 20, Last seq
16-OCT-2001 (Rel. 40, Last anno
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27.6%;
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                  32; Conservative
                                               VPFLLNL----FLGF---
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Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 LFALGTLAGFGTASRV--LGNGARPMRWSAGCTDRVPGFVAIIMSSLISQDGIWLFLAGT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 F-LGFGIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=RCR2011 / SU47;
MEDLINE=9000873; PubMed=2551890;
Bngelke T., Jording D., Rapp D., Puehler A.;
"Identification and sequence analysis of the Rhizobium meliloti dctA
gene encoding the G4-dicarboxylate carrier.";
J. Bacteriol. 171:5551-5560(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 IFVLATFCVFSSFAQANDSKNGAFGM--SAG-----EKLLVYETSKQDPIVPFLLNL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 FAVGLGIGLFGHATLTATMRTAPADRIGLAL---GAWGAVQA-----TAA-----GLGV
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Conservation between coding and regulatory elements of Rhizobium
mellloti and Rhizobium leguminosarum dct genes.";
J. Bacteriol. 171:5244-5253(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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BFC7A8A0C549875A CRC64;
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15-JUN-2002 (Rel. 41, Last annotation update)
C4-dicarboxylate transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCTA OR RB1523 OR SMB20611.
Rhizobium meliloti (Sinorhizobium meliloti).
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MEDLINE=90008755; PubMed=2793824;
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(Rel. 17, Last seq
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29.18;
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SEQUENCE FROM N.A.
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P20672;
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                                                                                                                                                                                                  Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Herrandez-Lucas I., Becker A., Cowle A., Gouzy J., Golding B., Puchler A.;
"The complete sequence of the 1,683-kb psymB megaplasmid from the N2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001991; Na/diCO_symp.
Pfam: PF00375; SDF: 1.
PROSITE; PS00713; Na_DICARBOXYL_SYMP_1; 1.
PROSITE; PS00714; Na_DICARBOXYL_SYMP_2; 1.
Transport; Sugar transport; Transmembrane; Inner membrane; Symport;
                                                                                        fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
Plant Microbe Interact. 3:174-181(1990).
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                                                                                                                                                                                                                                                                                                   been used in orthologous entries.
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=1021;
MEDLINE=21396508; PubMed=11481431;
                                                                                                                                 MEDLINE=94049668; Pubmed=8232193;
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M26531; AAA26248.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid; Complete proteome.
                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191
                                                                                                                       TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEM
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PERIPLASMIC.

DOMAIN TRANSMEM

FRANSMEM

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SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
                                                                                                                                                                           NLFLGFGIGSFAQGDIL-----GGSL-ILGFDAVGIGLILAGAYLDIKALDGITKK 103
                                                                                                                                                                                                                                                                                        NIIPTTLVGAFAEGDILQVLFISVLFGISLAIVGKKAEPVVDFLQALTLPIFRLVAILMK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Responsible for the transport of dicarboxylates such as minding functions for and malate from the periplasm across the
                                                                                                                                                        3 KLLIFVLA--TFCVFSSFAQANDSKNGAFGMSA-----GEKLLVY-ETSKQDPIVPFLL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             van Slooten J.C., Bhuvanasvari T.V., Bardin S., Stanley J., "Two C4-dicarboxylate transport systems in Rhizobium sp. NGR234: rhizobial dicarboxylate transport is essential for nitrogen fixation in tropical legume symbloses.";
Mol. Plant Microbe Interact. 5:179-186(1992).
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97305956; PubMed-9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                       104 A-----AFQWTWGKGVMLAGVVTWAVTRLTEIILPFTFA------NSYN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Freiberg C., Perret X., Broughton W.J., Rosenthal A.; "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium NGR234 using dye terminators and a thermostable 'sequenase': a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
                                                                                                    Length 441;
                                                                                                                                Indels
                                                                        B926FE7E3DC8B67D CRC64;
                                                                                                                               72;
                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          P31601; Q53214;
01-JUL-1993 (Rel. 26, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
C4-dicarboxylate transport protein.
                                                                                                                ed. No. 7;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   497 AA.
                                                                                                 Score 80.5;
Pred. No. 7;
  CYTOPLASMIC.
                               PERIPLASMIC.
                                                        CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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SEQUENCE FROM N.A.
MEDLINE=96389014; Pubmed=8796346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92314432; PubMed-1617199;
                                                                                                                             25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium sp. (strain NGR234).
                                                                       46142 MW;
                                                                                                8.98;
                                                                                                             27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6:590-600(1996)
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobiaceae; Rhizobium
378
398
405
424
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RYIKEELLLVLG 275
                                                                                                                                                                                                                                                                                                                                RKLKNSLNVALG 153
                                                                       441 AA;
                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DCTA1 OR Y4VF.
                                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DCTA_RHISN
DOMAIN
TRANSMEM
                               DOMAIN
TRANSMEM
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                                                                       SEQUENCE
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Best Local
                                                         DOMAIN
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                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                             PVETMSGLSSQRSDTVELGQKVLFGATNSADRTLAGRPGGR
DSRRIAPDHSAQVFGGPLSL -> AGGDHVGVVKPAE (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 AAPIGAFGAMAFTIGKYGV--ASIANLAMLIGTFYLTSFLFVFMVLGAVARYNGFSIVAL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 NLFLGFGIGSFAQGDIL------GGSL-ILGFDAVGIGLILAGAYLDIKALDGITKK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KLLIFVL---ATFCVFSSFAQANDSKNGAFGMSA-----GEKLLVY-ETSKQDPIVPFLL 53
(SDF, TC 2.A.23).
CAUTION: There are two genes for DctA in NGR234; one on the symplasmid, the other on the chromosome.
                                                                                                                                                                                                                                                                   Inner membrane; Symport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 A-----AFQWTWGK-GVMLAGVVTMAVTRLTEIILPFTFA------NSYN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49E960D8845B2824 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  T -> A (IN REF. 1).
A -> G (IN REF. 1)
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
MPN096 OR MP058.
                                                                                                                                                                                                                      Prom; PF00375; SDF; 1.
PROSITE; PS00713; NA_DICARBOXYL_SYMP_1; 1.
PROSITE; PS00714; NA_DICARBOXYL_SYMP_2; 1.
Transport; Sugar transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.9%; Score 80.5; DE 26.9%; Pred. No. 7.9; tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                               POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                    ALT_INIT.
                                                                                                                                                           EMBL; S38912; AAB22400.1; ALT_INIT.
EMBL; S38912; AAB22401.1; -.
                                                                                                                                                                                   EMBL; Z68203; CAA92421.1; ALT_INIT.
EMBL; AE000101; AAB91894.1; ALT_INI
INTERPTO; IPR001991; Na/diCO_SYMP.
Pfam. PF00375; SDF; 1.
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SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                          45
82
1117
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227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 IRYIKEELLLVLG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  497 AA;
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                                                                                                                                                                                                                                                                                          27
60
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P75596;
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Synechococcus sp.
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Q55038;
                                                                                                                                                                                                                                                                           Transport
TRANSMEM
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                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseefib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                              "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 GIGSFAQGDILG-GSLILGFDAVGI----GLILAGAYLDIKALDGITKKAAFQWTWGKGV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 GKGFKSMGCLLEFADLIATWTSVGIFWFLGLVLLGGLLQIKK----PKRWYFRTTGWLAV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: Polyketide antibiotic tetracenomycin C biosynthesis.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
AS THE DRUG RESISCHANCE TRANSLOCASE FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBL_TaxID-1907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 174:3651-3658(1992).
-!- FUNCTION: RESISTANCE TO TETRACENOMYCIN C BY AN ACTIVE
TETRACENOMYCIN C FEFLUX SYSTEM WHICH IS PROBABLY ENERGIZED BY
TRANSMEMBRANE ELECTROCHEMICAL GRADIENTS.
                                                                                              Nucleic Acids Res. 24:4420-4449(1996).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: TO THE C-TERMINAL SECTION OF M.PNEUMONIAE MPN308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glaucescens tcmAR tetracenomycin C resistance and repressor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                     Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN-ATCC 13032 / ETH 22794 / GLA.0;
MEDLINE-927347; Pubmed-1592819;
Guilfolle P.G., Hutchinson C.R.;
"Sequence and transcriptional analysis of the Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Indels
                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84F1B7716ACB928F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 MLAGVVTMAVTRLTEIILPF-----TFANSYNRKLKNSLNVAL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petracenomycin C resistance and export protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 80;
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MEDLINE=97105885; PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000007; AAB95706.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 31, Created)
(Rel. 31, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28961 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces glaucescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                21
63
115
166
201
235
                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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15-JUN-2002
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                                                                                  pneumoniae.
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P39886;
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TCMA_STRGA
TDMA_STRGA
DT 01-FEB
DT 15-FEB
DT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 KA------GVMLAGVV----TMA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 RAERAPKSFDVSGIVLLSGAMFCLVWGLIKAPA--WGWGDLRTLGFLAAAVLAFAGFTLR 262
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Liu Y., Tsinoremas N.F., Golden S.S., Kondo T., Johnson C.H.;
Circadian expression of genes involved in the purine biosynthetic
pathway of the cyanobacterium Synechococcus sp. strain PCC 7942.";
Mol. Microbiol. 20:1071-1081(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Amidophosphoribosyltransferase precursor (EC 2.4.2.14) (Glutamine phosphoribosyltyrophosphate amidotransferase) (ATASE) (GPATase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 PFLLNLFLGFGIG----SFAQGDILGGSLI--LGFDA-----VGIGLILAGAYL--DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
                                                                                                                                                                                                                                                            TIGRFAMs; TIGR00711; efflux_EmrB; 1.
Antibiotic resistance; Antibiotic biosynthesis; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (strain PCC 7942) (Anacystis nidulans R2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.9%; Score 80; DB 1; Length 538; 25.7%; Pred. No. 9.4; 1. Indels 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: De novo purine biosynthesis; first step. SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
DED3F28C1F22AA56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             493 AA.
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POTENTIAL.
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                                                                                                                                                                                     InterPro; IPR004638; Efflux_EmrB.
InterPro; IPR003662; sub_transporter.
                                                                                                                                                                                                                                   Pfam; PF00083; sugar_tr; 1.
TIGRFAMs; TIGR00711; efflux_EmrB;
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Μ.
                                                                                                                EMBL; M80674; AAA67509.1; -.
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1120
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1174
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306
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344
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494
538 AA;
                                                                                                                                      PIR; S27687; S27687
PIR; A41901; A41901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 35; Conserv
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CBHB OR CENE
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                                                                                                                                                                                                                                               InterPro;
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GUXB_CELFI
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                                       ween the Swiss Institute of Bioinformatics and the EMBL outstation
European Bioinformatics Institute. There are no restrictions on it
by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                            59 FGIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIK--ALDGITKKAAFQWTWGKGVML 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AGVVTMAVTRLTEIILPFTFAN----SYNRKLKNSL------NVALGGFEPSFDVAM 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 APQPKLCVFEMIYFARPDSLFHGESLYSYRRRIGQRLAKEAPADVDLVLGVPDSGIPAAI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 NGQTRY-----VLSSETCGLDIIGADYVRDIAPGEMVRITDAGLESWTWAE---- 261
                                                                                                                                                                                                                                                                                                                                                                                                          LATFCVFSSFAQAND----SKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLG 58
 SIMILARITY: CONTAINS 1 TYPE-2 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 392:353-358(1998).
-1- FUNCTION: PHOSPHORYLASE IS AN IMPORTANT ALLOSTERIC ENZYME IN
                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 493;
                                                                                                                                                                                                                                                                                                         AMIDOPHOSPHORIBOSYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                    27 GATASE (BY SIMILARITY).
53809 MW; E03508F8A922910C CRC64;
                                                                                                                                                                                                                            TIGREAMS; TIGRO1134; purF; 1.
PROSITE; PSO103; PUR_PYR_PR_TRANSFER; FALSE_NBG.
PROSITE; PSO0443; GATASE_TYPE_II; FALSE_NBG.
Purine blosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
Glycogen phosphorylase (EC 2.4.1.1).
                                                                                                                                                                                                                                                                                                                                              8.8%; Score 79.5; DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 692 AA.
                                                                                                                                                                                                                                                                                                                                                                  ilarity 21.4%; Pred. No. 9.5;
Conservative 25; Mismatches
                                                                                                                                                                               InterPro; IPR000836; PRTransferase.
InterPro; IPR002375; Pr/py_rp_transf.
Pfam: PF00156; Pribosyltran; 1.
Pfam: PF00310; GATase_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98196666; Pubmed=9537320;
                                                                                                                                                                  InterPro; IPR000583; GATase_2.
                                                                                                                          EMBL; U33211; AAA75107.1; -.
HSSP; P00497; 1AO0.
MEROPS; C44.001; -.
                                                                                                                                                                                                                                                                                 Glutamine amidotransferase.
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                                                                                                                                                                                                                                                                                                                                493 AA;
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 GOSSALG 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 GFSEALG 328
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SEQUENCE
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PHSG_AQUAE
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CARBOHYDRATE METABOLISM. ENZYMES FROM DIFFERENT SOURCES DIFFER IN THEIR REGULATORY MECHANISMS AND IN THEIR NATURAL SUBSTRATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 YEDIYKKPIV-FLSPEYGLHHTLLIYAG-GLG-FLAGDILKESSDLGFPLIGVGFMYPQG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 YL------GV--VTMAVT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 YVKQRIRVDGWQEDLDAQNQKELMPVKKVLDKEGKWLKCYVYVRDEKVYFGVWEVNVGKT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                             HOWEVER, ALL KNOWN PHOSPHORYLASES SHARE CATALYTIC AND STRUCTURAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Glycosyltransferase; Carbohydrate metabolism; Oglycogen metabolism; Pyridoxal phosphate; Complete proteome. BINDING 586 586 PYRIDOXAL PHOSPHATE (BY SIMILARITY). SEQUENCE 692 AA; 81158 MW; 4DC0EA2B2ESBBEA4 CRC64;
                                                                                                                                                          CATALYTIC ACTIVITY: {(1,4)-alpha-D-glucosyl}(N) + phosphate . (1,4)-alpha-D-glucosyl}(N) + alpha-D-glucose 1-phosphate. CCFACTOR: PYRIDOXAL PHOSPHATE (HY SIMILARITY).
SIMILARITY: BELONGS TO THE GLYCOGEN PHOSPHORYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Exoqlucanase B precursor (EC 3.2.1.91) (Exocellobiohydrolase (1,4-beta-cellobiohydrolase B) (CBP120).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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Biochem. J. 311:67-74(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.8%; Score 79.5; I
25.9%; Pred. No. 13;
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MEDLINE=96003898; PubMed=7575482;
                                                                                                                         PROPERTIES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000704; AAC06896.1; -.
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                                                          A Shen H., Tomme P., Meiner A., Gilkes N.R., Kilburn D.G.,
Warren R.A.J., Miller R.C. Jr.; Gilkes N.R., Kilburn D.G.,
Warren R.A.J., Miller R.C. Jr.; Gilkes N.R., Kilburn D.G.,
Warren R.A.J., Miller R.C. Jr.; Gilkes N.R., Kilburn D.G.,

"Stereochemical course of hydrolysis catalysed by Cellulomonas fimi
Cent. a member of a new family of beta-1,4-glucanases.";
Biochem. Biophys. Res. Commun. 199:1223-1228(1994).

"FONCTION: HYDROLYSE CELLOHERAGSE TO A MIXTURE OF CELLOTETRAOSE,
CELLOTRIOSE AND CELLOBIOSE, MITH ONLY A TRACE OF GLUCOSE. IT
HYDROLYSED CELLOPENTAOSE TO CELLOTRIOSE AND CELLOPINSE AND CELLOPINSES CELLOTRIOSE.

"HAS ALSO WEAK ENDOCLICANASE ACTIVITY. HYDROLYSES GLUCOSIDIC BONDS
WITH INVERSION OF ANOMERIC CONFIGURATION.

"I CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
In cellulose and cellotetraose, releasing cellobiose from the non-reducing ends of the chains.

"I SIMILARITY: CONTAINS 3 FIBRORECTIN TYPE III-LIKE DOMAINS.

"I SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 AVTRLTEIILPFT-----FANSYNR-----KLKNSLNVALGGFEPSFDVAMGQSSA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO CELLULASE FAMILY L (FAMILY 48 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | R Prodom; PROSTE; PROPE; PROSTE; PROPE; PROSTE; PROPE; PROSTE; PROPE; PROSTE; PROPE; PROSTE;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXOGLUCANASE B.
CATALTIC (BY SIMILARITY).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
CELLUOSE-BINDING (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.8%; Score 79; DB 1; Length 1090;
24.6%; Pred. No. 23;
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InterPro; IPR001961; FN_III.
InterPro; IPR003962; FN_III.
InterPro; IPR000362; FNIII.repeat.
InterPro; IPR000556; Glyco_hydro_48.
Pfam; PF00041; fn3; 3.
Pfam; PF00553; CBM_2; 1.
Pfam; PF02011; Glyco_hydro_48; 1.
PRNYTS; PR00014; FNYPEIII.
PRNYTS; PR00044; GLHYDRLASE48.
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513 513 NUCLE
990 1089 BY SI
1090 AA; 114829 MW; C
                     SEQUENCE OF 54-78.
MEDLINE-94197708; PubMed-8147863;
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nes 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-9834137; PubMed-9679194; MEDLINE-9834137; PubMed-9679194; MEDLINE-9834137; PubMed-9679194; MEDLINE-9834137; PubMed-9679194; Mawarabayasi Y., Sawada M., Horikawa H., Haskawa Y., Hino Y., Yamanoto S., Sekine M., Baba S.-I., Kosuqi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Sakai M., Ogura T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.; "Complete sequence and gene organization of the genome of a hyper-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 TSKQDPIVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILA-GAYLDIKALDGI 100
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                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1938).
-!- SIMILARITY: BELONGS TO THE CDP-ALCOHOL PHOSPHATIDYLTRANSFERASE
CLASS-I FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 8.6%; Score 78; DB 1; Length 188; Local Similarity 29.0%; Pred. No. 5.1; nes 40; Conservative 15; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP000002; BAA29546.1; -.
InterPro; IPR000462; CDP-OH_P_transf.
Pfam; PF01066; CDP-OH_P_transf; 1.
PROSITE; PS00379; CDP_ALCOHOL_P_TRANSF; 1.
Hypothetical protein; Transferase; Complete proteome.
SEQUENCE 188 AA; 20418 MW; D7FE6234216D3214 CRC64;
                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
188 AA
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                                                                                                                                                                                Hypothetical protein PH0460.
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SYSRCRAELAGSGTLAIG 139
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STANDARD;
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March 14, 2003, 14:22:51 ; Search time 24.47 Seconds
  (without alignments)
  1507.249 Million cell updates/sec
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902
1 MNKLLIFVLATFCVFSSFAQ......DVAMGQSSALGFELSFKKSY 179
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Inimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_human:*
sp_invertebrate:*
sp_anminal:*
sp_mammal:*
sp_organelle:*
sp_phage:*
sp_phage:* sp_virus:* sp_vertebrate:* sp_unclassified:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:* sp_rodent:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O51065 borrelia bu	Q9x3u9 borrelia af	Q9x3v0 borrelia qa	O50896 borrelia bu	O50885 borrelia bu	Q9s011 borrelia bu	O50696 borrelia bu	031325 borrelia bu	Q93re6 vibrio para	Q8uav6 agrobacteri	Q98kk8 rhizobium 1	Q9kxk6 streptomyce	Q976y7 sulfolobus	Q92mi7 rhizobium m	033763 streptococc	Q55742 synechocyst
SUMMAKIES	QI.	051065	60x30	Q9X3V0	050896	050885	098011	969050	031325	Q93RE6	Q8UAV6	Q98KK8	Q9KXK6	Q976Y7	Q92MI7	033763	055742
	BB :	16	7	7	16	16	7	16	7	7	16	16	16	17	16	7	16
	% Query Hatch Length DB	179	178	177	161	170	161	190	95	427	616	198	289	442	462	1874	214
	& Query Match	100.0	85.3	81.7	32.3	31.0	27.4	26.1	17.2	10.5	10.1	9.7	9.7	9.7	9.7	9.6	9.5
	Score	902	769.5	737	291	279.5	247.5	235	155.5	94.5	91	87.5	87.5	87.5	87.5	86.5	98
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17 86 9.5 274 16 Q8XQB4 18 86 9.5 303 2 Q93RD3 2		Q9h122 thermoplasm P73160 synechocyst Q9rg4 bacillus ps 087858 streptomyce Q8vs09 klebsiella Q9r637 rhodobacter Q9pnal campylobact Q9r141 rattus norv Q97a18 thermoplasm Q92s78 rhizoblum m Q97re5 streptococc Q9a523 caulobacter P73100 synechocyst O33762 streptococc
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ALIGNMENTS

RESULT 1 051065	O51065 PRELIMINARY O51065;	(TrEMBLrel.	20,			Bacteria; Spirochaetales; Spirochaetaceae; Borrelia. ′NCBI TaxID=139;			STRAIN=ATCC 35210 / B31; wepring_oogsous: p.:hwad_oogses.		Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,				Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,				Durgaorieti,	Marule 350:360-360(1557);	SEQUENCE FROM N.A.	STRAIN=ATCC 35210 / B31;	Noppa L., Ostberg Y., Bergstrom S.;	"P13, a novel integral membrane protein of Lyme disease Borrelia.";	Submitted (AUG-1998) to The EMBL/GenBank/DDBJ databases. Empt. Neoniii Nooceast	EMBL; AEOUIII; AACO04Z0.1; FMRL; AF085739: AAD28360.1;		Hypothetical protein; Complete proteome.	112 PAR, 13104 PAR,
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Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., Viterback R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                  IGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 ---MLAGV-VTMAVTRLT-EIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSAL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNKLLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFG 60
                                                                                                                                                                                                                                                       TMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSALGFELSFKKSY 179
                                                                                                                                                                                                                                                                                                                                                                                                                   4 LLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFGIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 FAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGV-----
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EMBL; AF085741; AAD28362.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 161;
                                                                                                                                             Length 177;
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                                                                                                                                                                                      18; Indels
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161 AA; 17887 MW; D93BDB326FE2DA30 CRC64;
                                                                                                    177 AA; 19308 MW; 429928CC426E1111 CRC64;
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NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                             81.7%; Score 737; DB 2;
81.0%; Pred. No. 1.1e-57;
tive 14; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi (Lyme disease spirochete).
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39.5%; Pred. No. 3e-18;
tive 23; Mismatches 4
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STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    burgdorfer1.";
Nature 390:580-586(1997).
EMBL; AE000790; AAC66226.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein BBA01
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Best Local Similarity
Matches 75; Conserv
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                                                                                                       1 MNKLLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ပ်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                terminally processed and contains surface-exposed domains."; Infect. Immun. 69:3323-3334(2001). EMBL: AF08574(0), AAD28361.1; -... SEQUENCE. 179 %.
                                          ó
Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.3%; Score 769.5; DB 2; Length 178; 84.9%; Pred. No. 1.5e-60; 1ve 10; Mismatches 16; Indels 1
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia garinii.
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=29519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID=29518;
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Last annotation update)
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100.0%; Score 902; DB 16; 100.0%; Pred. No. 2.8e-72;
                                          Mismatches
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                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21189251; PubMed=11292755;
Noppa L., Ostberg Y., Lavrinovicha M.,
"Pl3, an integral membrane protein of B
                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Conservative
                                        Conservative
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Matches 152; Conserv
                   Similarity
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SEQUENCE FROM N.A.
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"A bacterial genome in flux: The twelve linear and nine circular extracthromosomal DNAs in an infectious isolate of the Lyme disease spirochete Borrelia burgdorferi.";
MOI. Microbiol. 0:0-0(1999).
Hypothetical protein; 11--
Hypothetical protein; 14D4906CC8107CD2 CRC64;
SEQUENCE 161 AA: 17016 MW;
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nes 56; Conserv
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SEQUENCE
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Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artlach P., Bowman C.,
Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Lathigra R.,
White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-Vugt R.,
Palmer N., Haft D., Rosa P., Stevenson B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSALGFELSFKKSY 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 170 AA; 18227 MW; 0E71B633EA80FB22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                Plasmid 1p28-4.
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.0%; Score 279.5; DB 36.9%; Pred. No. 3.4e-17; cive 29; Mismatches 69
                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                      Created)
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STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; Pubmed-9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      burgdorferi.";
Nature 390:580-586(1997).
EMBL; AEO00789; AAC66194.1; -
TIGR; BBI31; -
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170 GFELSFKKSY 179
                        152 GFQLSFKKSY 161
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                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=139;
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                                                                                                                                                                  050885
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SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
STRAIN-ATCC 35210 / B31;
Frabine 3. Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Fracer C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Ulterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                78 FDAVGIGLILAGAYL--DIKALDGITKKAAFQWTWGKGVMLAGV--VTMAVTRLTEIILP 133
                                                                                                                                                                                                                                                                                                  96 ALDGITKKAAFQWTWGKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 QMKNLKKEPAS--ISSMILLLSGMLTFGSSYLISIYLPVLFEDRYYKNLMNRIIDELAGF 171
                                                                                                                                                                   37 LLVYETSKQ-DPIVPFLLNLFLGFGIGSFAQGÖILGGSLILGFDAVGIGLILAGAYLDIK 95
                                                                                                                                  18 FAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLLNLFLGFGIGSFAQGDILGGSLILG
   Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H41; -.
Hypothetical protein; Complete proteome.
190 AA; 21813 MW; A80FB8BCAD4B13EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein BBH41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.1%; Score 235; DB 16; 1
llarity 38.9%; Pred. No. 3.3e-13;
Conservative 25; Mismatches 51;
27.4%; Score 247.5; DB 2;
40.9%; Pred. No. 2.2e-14;
tive 25; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                113 FKFANRYNADLKKRLGIALAGLEPNFDIGINGDS 146
                                                                                                                                                                                                                                                                                                                                                                                               FTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 EPNLDIGMN----GFQLSFKKSY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPSFDVAMGQSSALGFELSFKKSY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                burgdorfer1.";
Nature 390:580-586(1997).
EMBL; AE000784; AAC65989.1; -.
                                                                  63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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GI--TKKAAFQWTWGKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.1%; Score 91; DB 16; 22.2%; Pred. No. 7.4;
                                                                                                                           616 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.2%; Pred. No. 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE009255; AAL44077.1; -. EMBL; AE008358; AAK90129.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        616 AA; 63402 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 22.29
Matches 42; Conservative
                                                                                                                                                                                                                              Rhizobiaceae; Rhizobium.
                                           157 PSFDVAMGQSSALG 170
                                                                 235 -AYHAIMGOAGVOG 247
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 AMGQSSALG 170
                                                                                                                                                                                                                                        NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                       Nester E.W.;
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                                                                                                                                    Q8UAV6;
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                                                                                                   RESULT 10
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                                                                                                                                                                                                                                                                                                                                           5 LIFVLATFCVFSSFAQ----ANDSKNGAFGMSAGEKLLVYETSKQDPIV------ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 ----PFLLNLFLGFGIGS--FAQGDILGGSLILGFDAVG----IGLILAGAYLDIKALD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
                                                                                                                                                                                                                                                                                                         3;
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                                                                                                                                                                                                                                                                                  Length 95;
                                                                                                                                                                                                                 on the Borrelia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Akeda Y., Honda T.;
"Vibrio parahaemolyticus adhesin gene.";
"Vibrio parahaemolyticus adhesin gene.";
Submitted (ANG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB047560: BAB59008.1; -.
InterPro; IPR002528; MatE.
Pfam; PF01554; UPF0013; 2.
TIGRFAMS; TIGR00797; matE; 1.
SEQUENCE 427 AA; 45909 MW; 0B608B9DC70E3C71 CRC64;
                                                                                                                                                                                      MEDLINE-96305348; PubMed-8688460;
Feng S., Das S., Barthold S.W., Fikrig E.;
"Characterization of two genes, pl1 and p5, on the Bor
burgdorfer1 49-kilo base linear plasmid.";
Blochim. Blophys. Acta 1307:270-272(1996).
EMBL: L41151; AAB62281.1; ...
SEQUENCE 95 AA; 10739 MW; D12F6791F8920C3A CRC64;
                                                                                                                                  Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
                                                               01-JAN-1998 (TIEMBLrel. 05, Created)
01-JAN-1998 (TIEMBLrel. 05, Last sequence update)
01-DEC-2001 (TIEMBLrel. 19, Last annotation update)
(clone 8) s3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                17.2%; Score 155.5; DB 2;
41.5%; Pred. No. 1.6e-06;
tive 12; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72;
                                                                                                                       Borrelia burgdorferi (Lyme disease spirochete)
                                          95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                       58 IGSFVQGDYIGGGSVLGFNLLG 79
                                                                                                                                                                                                                                                                                                                                                                          61 IGSFAQGDILGGSLILGFDAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21, Adhesin.
                                                                                                                                                                                                                                                                                                       34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 25.8
es 50; Conservative
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio parahaemolyticus
                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=139;
                                                                                                                                                                                STRAIN=N40
                                                                                                                                                                                                                                                                                 Query Match
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MEDLINE-2160851; PubMed=11743194; Miller N., Blanchard M., Godoner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; Gurson J., Lomo C., Sear C., Strub G., Grielo C., Slater S.; Aprobacterium tumefaciens CS8."; Science 294:2323-2328(2001).
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Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Slang S., Yoo H., Tao Y., Bille P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 -----TWGKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 LATFCVFSSFAQANDSKNGAFGMSAGEKLLVYE------TSKQDPIVP----
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ABC transporter, membrane spanning protein.
ATU3261 OR AGR_L_3113
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
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187 GYLWLKKHIIAFGWGD--IRASLVLDKITRFLSLSLPTTF----
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Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor F
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;
                                                                "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Mature 417:141-147(2002).
EMBL; AL357591; CAB93434.1; -.
SEQUENCE 289 AA; 29123 MW; 89AD68D9D805BE10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                  Match 9.7%; Score 87.5; DB 16; Local Similarity 32.6%; Pred. No. 6.2; es 31; Conservative 12; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75;
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                                                                                                                                                                                                                                                                                                                                                                                130 IILPFTFANSYNRKLKNSLNVA---LGGFEPSFDV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442 AA
                                                                                                                                                                                                                                                                                                                                                                                                                         64 VVV-----NRAMPQPKKVAGLDLGQFGIAFTV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.7%; Score 87.5; D
Best Local Similarity 22.8%; Pred. No. 10;
Matches 47; Conservative 29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-JCM 10545 / 7;
PubMed-11572479;
Kawarabayasi Y., Hino Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=111955;
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                                                                                                                                                                                                                                                                                                                                                                                           FTRAIN WAFF303099;
MEDLINE-21082930; PubMed-11214968;
MEDLINE-21082930; PubMed-11214968;
Maneko T., Nakamura Y., Sato S., Kaneko T., Ramando A., Idesawa K., Ishikawa A., Kawashina K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 KK------ILLPFTFANSY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 VPFLLNLFLGFGIGSFAQGDILG-GSLILGFDAVGIGL-ILAGAYL-----DIKALDGIT 101
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                                                                                                                                                                                                                                                              Rhizobium lot1 (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL; AP002997; BAB48806.1; -.
InterPro: IPPR001123; LysE.
Pfam; PF01810; LysE; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 198 AA; 21126 MW; 67E14425F0ZE7DAB CRC64;
                                                                                                                                                    01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein mll1430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S : : | | | | : | | | | | SVSVWAGFGTALRGFLSDPVRLKWFNIAMG 186
                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative integral membrane protein. SCO2314 OR SCC53.05.
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Best Local Similarity 30.08
Watches 45; Conservative
                                                                                                               PRELIMINARY;
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  470 SAGEAAAIG 478
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                              RESULT 11
Q98KK8
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Sekine M., Baba S. I., Ankai A., Kougi H., Jin-no K., Takahashi M., Sekine M., Baba S. I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Coshima T., Kikuchi H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 PIYAVVGIFAPILIILVRLAEGFFVGGVTAGSHTIGPESVPERHRGWVGG---IGFSAAG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 IGLILAGAYLDIKALDGITKKAAFQWTWGKGVM-LAGVVTMAVTRLTEIILP----FTFA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LLIFVLATFCVF-SSFAQANDSKNGA--FGMSAGEKL------LVYETSKQD-- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------PIVPFLLNLFLGFGIGSFAQGD-----ILGGSLILGFDAVG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sulfolobus tokodaii.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55;
Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
EMBL; AP000981; BAB65009:1; -.
InterPro; IPR003662; sub_transporter.
Hypothetical protein; Complete proteome.
SEQUENCE 442 AA; 47602 MW; C7932E5ABF20F03A CRC64;
                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 LPRDATTAMGAALAAAXVTTLGQFVTWAWRLGRHYVRGPWKIELGRWLSVSLPIFLVDGF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 FLINLFLG-FGIGSFAQGDILGGS------LILGFDAVGIGLILAG 89
                                                                                                                                                                                                                                                                                       Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Backer A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau B., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
Analysis of the Chromosome sequence of the legume symbiont
Proc. Natl Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL. ALS91191; CAC47208.1;
EMBL. ALS91191; CAC47208.1;
EMBL. ALS91191; CAC47208.1;
EMPLOTE CALL ACAD. AS 49058 MW; GEBEB9B4CE96F14F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A comprehensive genetic study of streptococcal immunoglobulin Al proteases: evidence for recombination within and between species."; Infect. Immun. 66:181-190(1998).
EMBL: V13459; CaA73856.1; -.
MEROPS; M26.001; -.
InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Streptococcus. NCBL_TaxID=1305;
                                                                                                                                                               Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98084472; Pubmed-9423856;
Poulsen K., Reinholdt J., Jespersgaard C., Boye K., Brown T.A.,
Hauge M., Kilian M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical transmembrane protein SMC00743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
IgAl protease (EC 3.4.24.13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
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                                                        462 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1874 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.7%; Score 87.5; 25.9%; Pred. No. 11
                                                        PRT;
                                                                                                                                                                                                                                                                           MEDLINE=21396507; PubMed=11481430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 GFLLTNSDVVIVGLYLKPDDVAV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 25.9%
Matches 37; Conservative
                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus sanguis.
                                                                                                                                                    R02629 OR SMC00743.
                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
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                                                                        Q92MI7;
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                         RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 V-----GGGLILSVDALENGILL------QYNAEYQVSAGESLPSPGEI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 T------MAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSALG 170
                                                                                                                                                                                                                                                                                                                                                                                                                            83 LVYRLNSNTGAKTLPNTGDSNNSNTMMTAGLLTTIGLVVFVVSKRKVQSKFLLTVLVGGG 142
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                     5 LIFVLATFCVFSSFAQANDSKNGAFGMSAG----EKLLVYETSKQDPIVPFLLNLFLGFG
                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                         DB 2; Length 1874;
                                                                                                                                                                                                                                                                                                                64; Indels
                 Pfam; PF00746; Gram_Pos_anchor; 1.
TIGREAMS; TIGR01167; LPXTG_anchor; 1.
TIGREAMS; TIGR01168; YSIRK_Signal; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Hydrolase; Protease.
SEQUENCE 1874 AA; 207888 MW; FA30684926BB4532 CRC64;
                                                                                                                                                                                                                                                   Similarity 21.8%; Score 86.5; D Similarity 21.8%; Pred. No. 67; 11; Conservative 30; Mismatches
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InterPro; IPR000130; Zn_MTpeptdse
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                                                                                                                                                                                                                                                   Query Match
Best Local 9
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2003, 14:19:56; Search time 30.8258 Seconds (without alignments) 765.116 Million cell updates/sec Run on:

US-09-508-487-23 908 Perfect score:

1 MNKFLIFILVIFCAFSSFAQ......DINMGQASALGFGLSFKKSY 177 Sequence:

Scoring table:

908470 seqs, 133250620 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 Total number of hits satisfying chosen parameters:

Inimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_101002:*

// SIDS1/gogdata/geneseq/geneseqp_emb1/AA1989_DAT:
// SIDS1/gogdata/geneseq/geneseqp_emb1/AA1989_DAT:
// SIDS1/gogdata/geneseq/geneseqp-emb1/AA1990_DAT:
// SIDS1/gogdata/geneseq/geneseqp-emb1/AA1992_DAT:
// SIDS1/gogdata/geneseq/geneseqp-emb1/AA1993_DAT:
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// SIDS1/gogdata/geneseq/geneseqp-emb1/AA1996_DAT: /SIDS1/gcgdata/geneseg/genesegp·embl/AA1999.DAT:* /SIDS1/gcgdata/geneseg/genesegp·embl/AA2000.DAT:* /SIDS1/gcgdata/geneseg/genesegp·embl/AA2001.DAT:* /SIDS1/gcgdata/geneseg/genesegp-embl/AA2001.DAT:*/SIDS1/gcgdata/geneseg/genesegp-embl/AA2002.DAT:* /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
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/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Borrelia garinii T	Borrelia afzelii A	B. burgdorferi ant	Borrelia burgdorfe	B. burgdorferi ant	pll protein sequen	Borrelia burgdorfe	Novel mar regulate	Escherichia coli p	Botulism toxin hea
		ΙD		AAY04279	AAY19808	AAY04278	AAY19809	AAY04282	AAY04281	AAU29340	AAG98374	AAB04097
		DB	20	20	20	20	20	20	70	22	22	22
		Length	177	178	179	179	158	95	25	451	451	413
æ	Query	e Match Length DB I	100.0	9.98	81.2	81.2	73.5	18.8	12.2	6.7	9.7	9.6
		Score	806	786.5	737	737	667.5	170.5	111	88.5	88.5	87
,	Result	Ñ.		7	3	4	2	9	7	8	6	10

× u	Clostridium botuli Novel human diagno Novel human diagno Helicobacter pylor Porphorymonas ging Streptcoccus poly Propioniparienium	B. burgdorferi ant B. burgdorferi ant C. glutamicum SRT C glutamicum prote C. glutamicum prote C. glutamicum gl	Corynebacterium gl C glutamicum prote Novel human diagno H. pylori ORF (Sae H. pylori ORF (Sae Drosophila melanog Novel human diagno	Proplonibacterium E. coli 0-157 vero EHEC cae gene prod Amino acid sequenc H. pylori GHPO 132 Human transporter Eimeria tenella 45
AAB04082 ABG69077 AAW56018 AAY93308 AAY93311	AAW68392 ABG07111 ABG24514 AAU35869 AAX34545 ABP27264	AAY19965 AAY19964 AAB78998 AAG90173 AAB78997 AAE19943 ABP38116	AAB76781 AAG93096 ABG27217 AAW55463 AAW55244 ABB58293 ABG26754	AAU67004 AAR55119 AAR5552 AAR5550 AAW9808 AAE16782 AAW33621
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ALIGNMENTS

RESULT 1

140		AA.			Borrelia; P13 antigen; spirochaete; vaccine; infection; diagnosis.												Nucleic acid from Borrelia burgdorferi encoding virulence associated		
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	AAY04280	<pre>ID AAY04280 standard; Protein; 177 AA. XX</pre>							04-SEP-1998;	•	16-SEP-1997;	10-SEP-1997;	XX	XX				protein	

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WO9859071-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rabbit polyclonal antibody raised against a 13 kDa polypeptide of Borrella burgdorferi B131, but not reactive with most proteins from ther spirochaetes; and/or (ii) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most cother spirochaetes. (I), (II) and transformed cells are useful in vaccines to protect against infection by B. burgdorferi sensu lato. (I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The I3 kD protein is involved in virulence and is highly conserved within B. burgdorferi sensu lato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis, compared with use of whole bacteria as antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a Borrelia garinii IP90 protein. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNKFLIFILVIFCAFSSFAQDDSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFGIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid from Borrelia burgdorferi encoding virulence associated protein P13
                                                                                                                      present invention describes an isolated nucleic acid (I) that: (i) encodes a polypeptide fragment (II) immunologically reactive with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVTRLTEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 90%; DB 20;
100.0%; Pred. No. 3.4e-92;
Live 0; Mismatches 0;
Claim 31; Page 114-115; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia afzelii ACAI protein.
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97DK-0001041.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 177; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 AA;
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10-SEP-1997;
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present invention describes an isolated nucleic acid (1) that: (1) encodes a polypeptide fragment (II) immunologically reactive with encodes a polypeptide fragment (II) immunologically reactive with crabbit polyclonal antibody raised against a 13 kpa polypeptide of crabbit polyclonal antibody raised against a 13 kpa proteins from other spirochaetes; and/or (11) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most to specific nucleic against infection by B. burgdorferi sensu lato. (I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The 13 kp protein is involved in virulence and is highly conserved within B. burgdorferi sensu lato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 GSFAQGDILGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKADFKWTWGKGMMLAGVVT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 MAVTRLTEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Borrelia burgdorferi nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases
The present sequence represents a Borrelia afzelii ACAI protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.6%; Score 786.5; DB 20; Length
86.5%; Pred. No. 9.2e-79;
ive 7; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compared with use of whole bacteria as antigen.
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97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-189980/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX61505.
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                                                                       invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a Borrelia burgdorferi B313 protein. The present invention describes an isolated nucleic acid (I) that: (i) encodes a polypeptide fragment (II) immunologically reactive with rabbit polyclonal antibody raised against a 13 kDa polypeptide of Borrelia burgdorferi B313, but not reactive with most proteins from other spirochaetes; and/or (ii) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most
                                                                                                                                                                                                                                                                                                                                                            IGSFAQGDILGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKADFKWTWGKGMMLAGVV 118
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                             1 MNKFLIFILVIFCAFSSFAQ-DDSKS-TFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFG 58
                                                                                                                                                                                                                                                                                                 TMAVTRLTEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid from Borrelia burgdorferi encoding virulence associated
                                                            This sequence represents a Borrelia burgdorferi (Bb) protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrella; P13 antigen; spirochaete; vaccine; infection; diagnosis.
                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                 81.2%; Score 737; DB 20; Length 179; 81.0%; Pred. No. 2.7e-73; ive 14; Mismatches 18; Indels
caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 31; Page 108-109; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY04278 standard; Protein; 179 AA
                           Claim 12; Page 72; 275pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi B31 protein.
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97DK-0001041.
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N-PSDB; AAX30098.
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                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                     179 AA;
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10-SEP-1997;
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                                                                                                                                                                                                                                   Best Local Sim
Matches 145;
                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                         119
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          vaccines to protect dataset infection by B. burgdorferi sensu lato.
(I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The I3 kD protein is involved in virulence and is highly conserved within B. burgdorferi sensu lato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide ompared with use of whole bacteria as antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in
                                                                                                                                                                                                                                                                                                               59 IGSFAQGDILGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKADFKWTWGKGMMLAGVV 118
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                       119 TMAVTRLTEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        develop
                                                                                                                                                                                                                                                    1 MNKFLIFILVIFCAFSSFAQ-DDSKS-TFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFG
(II) and transformed cells are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to develo
                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigenic protein; vaccine; Lyme disease; infection; detection.
                                                                                                                                                                                          Length 179,
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Borrelia burgdorferi nucleic acids · used products for the diagnosis, prevention and treatment of caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                          18;
                                                                                                                                                                                          Query Match
81.2%; Score 737; DB 20;
Best Local Similarity 81.0%; Pred. No. 2.7e-73;
Matches 145; Conservative 14; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lathigra R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B. burgdorferi antigenic protein, t933.aa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY19809 standard; Protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanson MS,
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97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi GH, Erwin AL,
                                                                                                                                                              179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX61506.
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                                                                                                                                                                 Sequence
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AAY19809
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The present sequence

compared with use of whole bacteria as antigen. The prese represents a p11 protein sequence from a best hit search.

95 AA;

Sequence

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The present invention describes an isolated nucleic acid (I) that: (i) encodes a polypeptide fragment (II) immunologically reactive with rabbit polychothal antibody raised against a 13 kba polypeptide of crabbit polychothal antibody raised against a 13 kba polypeptide of crabbit polychothacter; balls, but not reactive with most proteins from cher spirochaetes; and/or (ii) hybridizes under stringent conditions of the spirochaetes. (I), (II) and transformed cells are useful in vaccines to protect against infection by B. burgdorferi sensu lato.

(I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi sensu lato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis,
                                                                                                                                                  ï
humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                         80 GIGLILTGAYLDIKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRLTEIVLPFTFANNYN 139
                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                     21 DDSKS-TFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid from Borrelia burgdorferi encoding virulence associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia; P13 antigen; spirochaete; vaccine; infection; diagnosis.
                                                                                                            DB 20; Length 158;
                                                                                                                                                14; Indels
                                                                                                                                                                                                                                                                                                                                                    140 RKLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177
                                                                                                          Query Match 73.5%; Score 667.5; DB 2
Best Local Similarity 82.3%; Pred. No. 1.1e-65;
Matches 130; Conservative 13; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 8; Page 118; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY04282 standard; Protein; 95 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0059036.
97DK-0001041.
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N-PSDB; AAX30115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYMB-) SYMBICOM AB
                                                                        158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bergstroem S;
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10-SEP-1997;
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The present sequence represents a Borrelia burgdorferi B313 N-terminal peptide. The present invention describes an isolated nucleic acid (I) that: (i) encodes a polypeptide fragment (II) immunologically reactive with rabbit polyclonal antibody raised against a 13 Kba polypeptide of Borrelia burgdorferi B313, but not reactive with most proteins from conter spirochaetes; and/or (ii) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most to specific nucleic against infection by B. burgdorferi sensu lato.

Crosporines to protect against infection by B. burgdorferi sensu lato.

(I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The I3 Kb protein is involved in virulence and is highly conserved within B. burgdorferi sensu lato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis, compared with use of whole bacteria as antigen.
                                    Gaps
                                                                    1 MNKFLIFILVIFCAFSSFAQDDSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFGIG 60
                                                                                         Nucleic acid from Borrelia burgdorferi encoding virulence associated
protein P13
                                                                                                                                                                                                                                                                                                                                                                                            Borrelia; P13 antigen; spirochaete; vaccine; infection; diagnosis.
                                    ä
     Length 95;
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                                    Indels
     DB 20;
18.8%; Score 1/0.5; LL., 45.0%; Pred. No. 4.6e-11; Live 11; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi B313 N-terminal peptide.
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                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                       AAY04281 standard; peptide; 25
                                                                                                                                      80
                                                                                                                                                       60 SFVQGDYIGGGSVLGFNLLG 79
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97DK-0001041.
                                                                                                                                      61 SFAQGDILGGSLILGFDAVG
                                                                                                                                                                                                                                                                                                                            (first entry)
                   Local Similarity 45.0%
Les 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia burgdorferi.
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10-SEP-1997;
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                                                                                                                                                                                                                                                                                          AAY04281;
      Query Match
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                      Best Loca
Matches
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(first entry)

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Escherichia coli; identification; proliferation; microorganism; antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis; bacterial growth inhibition.
                                                                                                           Escherichia coli protein sequence SEQ ID NO:422.
                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                WO200148209-A2.
                                                                21-SEP-2001
                                                                                                                                                                                                                                                                                                                           05-JUL-2001
                        AAG98374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of identifying compounds that modulate a newly identified mar regulated (NIMR) polypeptide activity. The method comprises contacting an NIMR polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulaters. NIMR nucleic acids and polypeptides are used in the treatment of microbial infections, and in screening for modulators of NIMR expression and activity. These modulators can be used to reduce the infectioity of a microbe on a surface, and the virulence of a microbe in a subject suffering from an infection. AAU29339-AAU39379 represent Escherichia coll NIMR amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying compounds that modulate a newly identified mar regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 LVPFLLNLF---LGFGIGSFAQCDILGGSLILGFDAVGIGLILTGAYLD-----IK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 MLPIVIIIFSKILG-----MKAGDCFKAGLHIGIGFVGIGLVI-GLMLDSIGPAAKAMAE 70
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                       mar regulated polypeptide; NIMR; microbial infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 DFDNNAKKADFKW-----TWGKGMMLAGV-----VTMAVTRLTEIV 129
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
  Pred. No. 3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Mismatches
                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.7%; Score 88.5;
27.5%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 203-205; 526pp; English.
                                                                                                                                                                                                                                                                                                                                             Novel mar regulated protein (NIMR) #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alekshun MN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG98374 standard; Protein; 451 AA
                                                                                                                                                                                                               AAU29340 standard; Protein; 451 AA
                                                                                    1 TSKQDPIVPFLENLFLGFGIGSFAQ 25
                                                              40 TNKKDSLVPFLLNLFLGFGIGSFAQ 64
84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2001; 2001WO-US07478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAR-2000; 2000US-188362P.
                                                                                                                                                                                                                                                                                                  18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Conservative
                      21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TUFT ) TUFTS COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barbosa TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-602769/68.
N-PSDB; AAS46240.
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200170776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001
                                                                                                                                                                                                                                                          AAU29340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Levy SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
AAG98374
ID AAG9
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The present invention describes a purified or isolated nucleic acid
sequence (I) consisting essentially of one of the 93 nucleotide sequences
given in AARB1202 to AARB1204, where expression of the nucleic acid in a
microorganism is capable of inhibiting proliferation of a microorganism.

(I) have antibacterial and antibiotic activities, and can be used in
gene therapy. Expression of (I) in a microorganism inhibits proliferation
of the microorganism, and the manufactured antibiotic is useful for
reducing the activity or level of a gene product required for
reducing the activity or level of a gene product required for
cucleic acids that inhibit bacterial growth or proliferation can be used
as antisense therapeutics for killing bacteria. In addition to
therapeutic applications, the nucleic acid sequences complementary to
sequences required for proliferation can be used as diagnostic tools.
For example, nucleic acid probes complementary to proliferation required
sequences that are specific for particular species of microorganisms can
be used as probes to identify particular microorganism species in
clinical specimens. AAHB1295 to AAHB1487 encode the Escherichia coll
proteins given in AAG98239 to AAG8431, and AAHB1488 to AAHB1480
represent oligonucleotides, which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 LVPFLLNLF---LGFGIGSFAQGDILGGSLILGFDAVGIGLILTGAYLD-----IK 93
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids encoding proteins required for Escherichia coll proliferation, useful for screening for antimicrobial agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFDNNAKKADFKW-----TWGKGMMLAGV------VTMAVTRLTEIV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.7%; Score 88.5; DB 22;
27.5%; Pred. No. 0.4;
ive 15; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 19; Page 543-544; 596pp; English
                                                                                                                                                                                                                                     Zyskind JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB04097 standard; Protein; 413 AA.
19-DEC-2000; 2000WO-US34419.
                                                                        99US-0173005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 27.5%
Matches 30; Conservative
                                                                                                                                                (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                     Ohlsen KL,
                                                                                                                                                                                                                                                                                                             WPI; 2001-457376/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 AA;
                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAH81430
                                                                        23-DEC-1999;
                                                                                                                                                                                                                                     Forsyth RA,
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282 ALNYQAQALEEIIKYRY-NIYSEKEKSNINIDFNDINSKLNEGINQA 327
                                                            AAB04082 standard; protein; 848
                                                                                                                                                                                                                                                                                                      99US-0133865.
99US-0133866.
99US-0133867.
99US-0133868.
                                                                                                                                                                                                                                                                                 12-MAY-2000; 2000WO-US12890.
                                                                                                                                                                                                                                                                                                                                                                  99US-0133873.
                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                           Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-016048/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          848 AA;
                                                                                                                                                                                                                                  WO200067700-A2
                                                                                                           11-APR-2001
                                                                                                                                                                                                                                                                                                      12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                             29-JUL-1999;
                                                                                                                                                                                                                                                          16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                   12-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                            Smith LA,
                                                                                                                                                                                    Infection.
                                                                                    AAB04082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                   RESULT 11
AAB04082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 VIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASILLEFIPELLIP 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 VVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 VYETNKKDS-----LVPFL---LNLFLGFGIGSFAQG-DILGGSLILGFD----AV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant expression vectors and expressed in transformed cells to produce peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressible in a recombinant organisms such as Escherichia coll or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from Clostridium botulinum serotypes A-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the
                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids encoding the carboxy· or amino-terminal portions the heavy chain of botulinum neurotoxin of serotype A-G, useful as vaccine against botulism
                                                                     heavy chain; recombinant expression; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 GIGLILTGAYLD----IKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRL-----
                                             Botulism toxin heavy chain N-terminal sequence (serotype B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQA 164
                                                                                                                                                                                                                                                                                                                                                     Middlebrook JL, Lapenotiere H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                             (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.6%; Score 87; DB 22
22.8%; Pred. No. 0.52;
Live 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Fig 12b; 73pp; English.
                                                                      Botulism; toxin; neurotoxin;
recombinant vector; antigen;
                                                                                                                                                                                                                                            99US-0133865.
99US-0133867.
99US-0133868.
99US-0133869.
                                                                                                                                                                                                         12-MAY-2000; 2000WO-US12890.
                                                                                                                                                                                                                                                                                         99US-0133873
                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 22.8% tes 38; Conservative
                                                                                                                     Synthetic.
Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                    Smith LA, Byrne MP,
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-016048/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 AA;
                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA54493
                                                                                                                                                        WO200067700-A2.
                                                                                                                                                                                                                                                                              12-MAY-1999;
12-MAY-1999;
29-JUL-1999;
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12-MAY-1999;
12-MAY-1999;
12-MAY-1999;
                      11-APR-2001
                                                                                                                                                                                 16-NOV-2000
                                                                    Botulism;
                                                                                             infection
AAB04097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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g
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New nucleic acids encoding the carboxy- or amino-terminal portions of
the heavy chain of botulinum neurotoxin of serotype A-G, useful as
vaccine against botulism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 GIGLILTGAYLD-----IKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRL------ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 VYETNKKDS-----LVPFL---LNLFLGFGIGSFAQG-DILGGSLILGFD----AV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide antigens useful for eliciting an immune response to give protective immunity against botulinum neurotoxin, which causes botulism. The nucleic acids are expressable in a recombinant organisms such as Escherichia coli or Pichia pastoris. The use of recombinant nucleic acids are advantageous since it eliminates the need to culture large quantities of hazardous toxin-producing bacterium. Production yield from the genetically engineered product is also high and cost of production is lower. The nucleic acids can be derived from Clostridium botulinum serotypes A-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Botulism neurotoxins are translated as a single 150 kDa polypeptide chain and then posttranslationally nicked, forming a dichain consisting of a 100 kDa heavy chain and a 50 kDa light chain which remain linked by a disulfide bond. Nucleic acids encoding the carboxy-terminal (HC) or amino-terminal (HN) portion of the heavy chain of botulinum neurotoxin (BoNT) can be used in recombinant expression vectors and expressed in transformed cells to produce
                                                                                    Botulism; toxin; neurotoxin; heavy chain; recombinant expression; recombinant vector; antigen; immune response; vaccine; bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lapenotiere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.6%; Score 87; DB 22; 22.8%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Mismatches
Botulism toxin heavy chain (serotype B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Byrne MP, Middlebrook JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 13; 73pp; English.
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the present invention. The present invention describes recombinant neurotoxin proteins which comprise a first and second domain, where the first domain is adapted to cleave one or more vesicle or plasma-membrane associated broteins essential to exocytosis, and where the second domain is adapted; (a) to translocate the protein into a cell; (b) to increase the solubility of the protein compared to the solubility of the first domain on its own, or (c) both to translocate the protein into a cell and to increase the solubility of the protein compared to the solubility of the first domain on its own, or (c) both to translocate the protein into a cell and to increase the solubility of the first domain on its own, the protein compared to the solubility of the first domain on its own, the protein being free of clostridial neurotoxin (CN) and free of CN precursor that can be converted into toxin by proteolytic action. The recombinant can be used as the protein and as non-toxic standards for the assessment and development in immunogens and as non-toxic standards for the assessment and development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vitro assays for the detection of functional botulinum or tetanus
                                                             601 VIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASILLEFIPELLIP 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a recombinant neurotoxin protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant neurotoxin polypeptides - used to develop therapeutic agents, immunogens or as non-toxic standards for the detection of neurotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurotoxins either in foodstuffs or in environmental samples
                                       GIGLILTGAYLD----IKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 858;
                                                                                                                                                                                                                                                                                                                                                                                                             recombinant; Clostridium botulinum; neurotoxin;
                                                                                                                 -----TEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQA 164
                                                                                                                                       721 ALNYQAQALEEIIKYRY-NIYSEKEKSNINIDFNDINSKLNEGINQA 766
                                                                                                                                                                                                                                                                                                                                                                                                                                 detection; tetanus; non-toxic; toxin.
                                                                                                                                                                                                                                                                                                                                                                     Recombinant botulinum neurotoxin type B LH417/B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.6%; Score 87; DB 19;
22.8%; Pred. No. 1.3;
iive 31; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 98-100; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MICR-) MICROBIOLOGICAL RES AUTHORITY. (SPEY-) SPEYWOOD LAB LTD.
                                                                                                                                                                                                                                                     AAW56018 standard; Protein; 858 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shone CC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96GB-0025996.
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                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 22.8<sup>†</sup>
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Foster KA, Quinn CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1998-169168/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           858 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-169168,
N-PSDB; AAV26290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9807864-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-1996;
                                                                                                                                                                                                                                                                                                                                 27-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                             Botulinum;
                                                                                                                                                                                                                                                                                                                                                                                                                                   rmmnoden;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                           AAW56018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a nucleic acid molecule encoding a botulinum neurotoxin light chain (BoNT LC) serotype A, where the DNA has a sequence that is expressible in a host organism other than clostridium, or has a total A+T content that is less than about 70% The BoNT LC protein is useful in vaccination against botulism, for eliciting protective immunity in a mammal, for treating dystonias, spasticity, pain, ocular motility, facial dyskinesias, stiff-person syndrome, bladder dysfunction, segmental myoclonus, hyperkinetic disorders, cosmetic treatment of facial wrinkles, conditions characterised by hyperactivity of the lower motor neuron, and to control autonomic nerve function or tiptoe-walking due to stiff muscles common in children with cerebral palsy. The sequences are also useful for screening for botulinum neurotoxin inhibitors. This sequence represents a botulinum neurotoxin light chain serotype A protein.
                                                                                                                                                                                                                                                                                                                                             Botulinum neurotoxin light chain; BoNT LC; botulism; dystonia; pain; spasticity; ocular motility; facial dyskinesia; stiff-person syndrome; bladder dysfunction; segmental myoclonus; hyperkinetic disorder; cosmetic treatment; facial wrinkle; cerebral palsy; analgesic; relaxant; lower motor neuron hyperactivity; autonomic nerve function; muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid molecule encoding botulinum neurotoxin light chain serotype A, useful for producing the neurotoxin for vaccination against botulism, comprises sequence expressible in host other than Clostridium
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LVPFL---LNLFLGFGIGSFAQG-DILGGSLILGFD----AV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.6%; Score 87; DB 23; Length 852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58; Indels
                                                       -----TEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQA 164
                                                                               281 ALNYQAQALEEIIKYRY-NIYSEKEKSNINIDFNDINSKLNEGINQA 326
                                                                                                                                                                                                                                                                                                           Botulinum neurotoxin light chain polypeptide #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>--</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 52; Page 138-139; 166pp; English.
                                                                                                                                                                                       ABG69077 standard; Protein; 852 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunostimulant; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2000; 2000US-246774P.
20-JUL-2001; 2001US-0910186.
09-AUG-2001; 2001US-311966P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001; 2001WO-US47230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.8%;
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium botulinum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-575192/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith LA, Jensen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               852 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 VYETNKKDS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABK98547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200236758-A2.
                                                                                                                                                                                                                                                                     07-0CT-2002
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                                                                                                                                                                                                                               ABG69077;
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                                                       126
                                                                                                                                                   RESULT 12
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37 VYETNKKDS-----LVPFL---LNLFLGFGIGSFAQG-DILGGSLILGFD----AV 79

-----TEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQA 164

126

80 GIGLILTGAYLD----IKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRL--

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The present sequence represents a construct of the invention, comprising a manganese superoxide dismutase (Mn.50) polypeptide, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype B. The specification describes a composition for delivery of 50D to neuronal cells. The composition comprises SOD linked, by a cleavable linker, to a neuronal cell targeting component (NCTC). This component has a domain that binds to a neuronal cell and a
                                                                        GIGLILTGAYLD-----IKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRL----- 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain that translocates the SOD of the composition into the neuronal cell. After translocation, the linker is cleaved to release the SOD. The composition is useful for treating neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma,
                                                                                                      662 VVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYK 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkinson's disease, Huntington's disease and motor neurone diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia
VYETNKKDS-----LVPFL---LNLFLGFGIGSFAQG-DILGGSLILGFD----AV
                      neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease; botulinum neurotoxin serotype B.
                                                                                                                                                                                                                                                                                                                                                                                                                  Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell;
                                                                                                                                                                  -----TEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQA 164
                                                                                                                                                                                                                                                                                                                                                                               A manganese superoxide dismutase (Mn-SOD) construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 45-47; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MICR-) MICROBIOLOGICAL RES AUTHORITY
                                                                                                                                                                                                                                                                     AAY93308 standard; protein; 1070 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hallis B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-GB03699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98GB-0024282
                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-376553/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1070 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shone CC,
                                                                                                                                                                                                                                                                                                          AAY93308;
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 37
                                                                                                                                             126
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The present sequence represents a construct of the invention, comprising a mitochondrial leader sequence from human manganese superoxide dismutase (Mn-SoD), a Bacillus stearothermophilus Mn-SoD, a linker that can be cleaved by thrombin, and a heavy chain derived from botulinum neurotoxin serotype B. The specification describes a composition for delivery of SoD to neuronal cells. The composition comprises SoD linked, by a cleavable linker, to a neuronal cell to a neuronal cell and a domain that translocates the SoD of the composition into the neuronal cell. After translocates the SoD of the composition into the neuronal cell. After translocates the subject is cleaved to release the SOD. The composition is useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuronal diseases caused or augmented by oxidative stress, such as ischemic stroke, trauma, Parkinson's disease, Huntington's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition, comprising superoxide dismutase linked by a cleavable linker to a neuronal cell targeting component useful for delivering superoxide dismutase to neuronal cells to treat ischemia
                                                                                                                                                                                                                               Manganese superoxide dismutase; Mn-SOD; SOD; neuronal cell; neuronal cell targeting component; NCTC; neuronal disease; oxidative stress; ischemic stroke; trauma; Parkinson's disease; Huntington's disease; motor neurone disease; botulinum neurotoxin serotype B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 1095;
A manganese superoxide dismutase (Mn-SOD) construct.
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Pred. No. 1.9;
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                                                                                               AAY93311 standard; protein; 1095 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hallis B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.6%;
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98GB-0024282.
                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sutton JM,
                                                                                                                                                                                                                                                                                                                                                                                     Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-376553/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1095 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200028041-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1999;
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                                                                                                                                                                04-SEP-2000
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                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                              AAY93311;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                               RESULT 15
                                                                             AAY93311
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Best Local Similarity

7;

Gaps

40;

58; Indels

31; Mismatches 9.6%; Score 87; D 22.8%; Pred. No. 1.

Conservative

Query Match Best Local Similarity Matches 38; Conserv

21; Length 1070;

DB

	Matches		38; Conservative 31; Mismatches 58; Indels 40; Gaps	31;	Mismatch	les 5		Indels	40;	Gaps	7;	
۵y		VYETNK		FLI	LNLFLGFGI	GSFAQG	-DILG	SGSLILGFD	ď	67 Vi		
đ		VIEANKSNTME	KIADIS	YIGLAI	II: LNVGNETAK	GNFENA	FEIAG	: :: LIVPYIGLALNVGNETAKGNFENAFEIAGASILLEFII	PELLI	P 465		
Ωy		GIGLIL	80 GIGLILTGAYLDIKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRL	DNNAK	KADEKWTWG	KGMMLA	GVVTÞ	AAVTRL		125		
q		WGAFL	466 VVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYK 525	DNALTE	I : II: KRNEKWSDM	I : : : I	OWLST	: VNTQFYTI	KEGMY	TK 525		
οy			126TEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGOA 164	NRKLK	NSLNIALGG	FEPSFD	INMGC	2A 164				
QQ		ALNYQA	526 ALNYQAQALEEIIKYRY-NIYSEKEKSNINIDFNDINSKLNEGINQA 571	SEKEK	SNINIDEND	INSKLN	EGINC)				

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TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA
FILE REFERENCE: 454312-3130.1
CURRENT APPLICATION INVERS: 05/05/153,447
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION NUMBER: 60/059,036
EARLIER FILING DATE: 1997-09-10
BARLIER FILING DATE: 1997-09-10
NUMBER: OF SEQ ID NOS: 31
SOFTWARE: PATENTIN Ver. 2.1
SOFTWARE: PATENTIN Ver. 2.1
SOFTWARE: DATE IN Ver. 2.1
STOID NO 20
TYPE: DNA
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Gaps

us-09-508-487-22.rnpm

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AATCAAGAAGCTCTATTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAAGTTAAATTTA 120
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Pred. No. 4.3e-97;
0; Mismatches 70;
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PRIOR FILING DATE: 1997-09-10
PRIOR APPLICATION NUMBER: 1041/9;
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
                                                                                                                                                             Query Match 81.0%;
Best Local Similarity 90.1%;
Matches 673; Conservative
                                                                                          ORGANISM: Borrelia afzelii
                                                                                                                         , LUCATION: (219)..(755)
US-09-156-447-20
                                                                                                                  NAME/KEY: CDS
LOCATION: (219
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US-09-508-487-20
                                                                                  TYPE: DNA
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                                                                     Length 862
                                                                                            Indels
                                                                   Score 607; DB 15;
Pred. No. 4.3e-97;
0; Mismatches 70;
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GENERAL INFORMATION:
APPLICANT: BERGSTROM, Sven
TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA
FILE REFERENCE: 454312-3130.1
CURRENT APPLICATION NUMBER: US/09/156,447
CURRENT FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/059,036
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90.1%;
  ORGANISM: Borrelia afzelii
                                                                   Query Match
Best Local Similarity 90.13
Matches 673; Conservative
                      ; NAME/KEY: CDS
; LOCATION: (219)..(755)
US-09-153-447-20
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US-09-156-447-20
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Pred. No. 1.6e-88;
0; Mismatches 88;
                                                                                                                            Sequence 18, Application US/09153447
GENERAL INFORMATION:
APPLICANT: BERGSTROM, Sven
; TILE OF INVENTION: P13 ANTIGENS FROM BORRELIA
; FILE REFERENCE: 454312-3130.1
; CURRENT APPLICATION NUMBER: US/09/153,447
; CURRENT FILING DATE: 1998-09-15
; EARLIER APPLICATION NUMBER: 60/059,036
; EARLIER PILING DATE: 1997-09-10
; BARLIER FILING DATE: 1997-09-10
; NUMBER: OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
                                                    747 AGTTATTAATTTTATTAAAA 773
                                        AGCTATTAATTTATTTAGAAAA 743
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ORGANISM: Borrelia burgdorferi
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ilarity 87.0%;
Conservative (
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; LOCATION: (170)..(709)
US-09-153-447-18
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Matches 638; Conserv
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Pred. No. 4.3e-97;
0; Mismatches 70;
                                        BORRELIA
                       APPLICANT: BERGSTROM, Sven
TITLE OF INVENTION: P13 ANTICENS FROM BORRE
FILE REFERENCE: 454312-3150
CURRENT APPLICATION NUMBER: 0S/09/508,487
CURRENT FILING DATE: 2000-03-10
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 20
Sequence 20, Application US/09508487 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         81.0%;
90.1%;
                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Borrelia afzelii
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Matches 673; Conservative
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; LOCATION: (219)..(755)
US-09-508-487-20
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677 CCAAGCIAGIGCICIIGGIIIIIGGACIGICIIIICAAAAAAAGCIAIIAAIIIIAIIC 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/09508487
GENERAL INFORMATION:
APPLICANT: BERGSTROM, Sven
TITLE OF INVENTION: P13 ANTICENS FROM BORRELIA
FILE REFERENCE: 454312-3150
CURRENT APPLICATION NUMBER: US/09/508,487
CURRENT FILING DATE: 2000-03-10
FRIOR FILING DATE: 1997-09-10
FRIOR FILING DATE: 1997-09-10
FRIOR FILING DATE: 1997-09-10
FRIOR FILING DATE: 1997-09-10
FRIOR APPLICATION NUMBER: PCT/IB98/01424
FRIOR APPLICATION NUMBER: PCT/IB98/01424
FRIOR APPLICATION NUMBER: PCT/IB98/01424
FRIOR APPLICATION UNMBER: PCT/IB98/01424
FRIOR APPLICATION NUMBER: PCT/IB98/01424
FRIOR APPLICATION UNMBER: PCT/IB98/01424
FRIOR APPLICATION UNMBER: PCT/IB98/01424
FRIOR PRICOR FILING DATE: 1998-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.5%; Score 558.2; DB 187.0%; Pred. No. 1.6e-88;
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US-09-508-487-18
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LOCATION: (170
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LENGTH: 759
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Pred. No. 1.6e-88;
0; Mismatches 88;
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CURRENT APPLICATION NUMBER: US/09/156,447
CURRENT FILING DATE: 1980-09-15
PRIOR APPLICATION NUMBER: 60/059,036
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1997-09-10
SOFTWARE: PATENTON NUMBER: 1041/97
PRIOR FILING DATE: 1997-09-10
SOFTWARE: PATENTON NUMBER: 21
SEQ ID NO 18
LENGTH: 759
                                                                                                                                                                                                                                                                                              ; Sequence 18, Application US/09156447; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Borrelia burgdorferi
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Best Local Similarity 87.0%;
Matches 638; Conservative
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US-09-156-447-18
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LOCATION: (170
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PCT-US98-12764-63

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Sequence 63, Application PC/TUS9812764
GENERAL INFORMATION:
APPLICANT: 611 Choi et. al.
TITLE OF INVENTION:
BOrrelia burgdorferi Polynucleotides and Sequences
NUMBER OF SEQUENCES: 155
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                                                                                                                    GTTAATACTTACAGGAGCTTATTTGGACATCAAGGATTTTGATAATAATGCTAAAAAGC 496
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                                                           TGCTCAAGGAGATATCCTTGGAGGTTCTCTTATTCTTGGATTTGATGCGGTTGGTATAGG
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB370PCT
TELECOMMUNICATION INPORMATION:
TELEPHONE: (301) 309-8504
TELEPKX: (301) 309-8512
INFORMATION FOR SEO ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MSDOS version 6. SOCTHWARE: ASCIT Text SOCTHERE: APPLICATION DATA: APPLICATION NUMBER: PCT/US98/12764
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9410 Key West Avenue
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TYPE: nucleic acid
STRANDEDNESS: double
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CITY: Rockville
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PCT-US98-12764-63/c
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APPLICANT: Gil Choi et. al.
TITLE OF INVENTION: Borrelia burgdorferi Polynucleotides and Sequences
NUMBER OF SEQUENCES: 155
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Length 1761;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: H9 Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
13.1%; Score 98.4; DB 1; 49.7%; Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 63, Application US/09830228 GENERAL INFORMATION:
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                              Conservative
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               Similarity
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US-09-830-228-63/C
                  Best Local Sim
Matches 336;
   Query Match
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS VERSION 6.2 SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                                  Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT/US98/12764
                                                                                                                       Sequence 14, Application PC/TUS9812764 GENERAL INFORMATION:
                                                                                                                                                                                                                                       ADDRESSEE: Human commenter: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INPERMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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      ||||||| ||| ||| ||| 377 ATTTTGACATTGGAAT 362
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SDNESS: double
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                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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STATE: Maryland
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 98.4; DB 32;
Pred. No. 1.4e-07;
0; Mismatches 331;
                                                                                                               APPLICATION NUMBER: PCT/US98/12764
FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                 APPLICATION NUMBER: US/09/830,228
FILING DATE: 24-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PB370PCT TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
                                                                                                                                                                                                REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                          LENGTH: 1761 base pairs
SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
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Best Local Similarity 49.7%;
Matches 336; Conservative (
                                                                                               PRIOR APPLICATION DATA:
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APPLICANT: Gil Choi et. al.
TITLE OF INVENTION: Borrelia burgdorferi Polynucleotides and Sequences
NUMBER OF SEQUENCES: 155
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7792 ACAAATAAACTTAAATCTCATACAACTGCACTTTTCGAACAACTTGATAAAAAAGAAGAC 7851
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT; Gil Choi et. al.
TITLE OF INVENTION: Borrelia burgdorferi Polynucleotides and Sequences
NUMBER OF SEQUENCES: 155
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                           8152 ATAGGATCCTTTGTTCAAGGAGATTATATTGGTGGTGGTGCACTACTTGGCTCTCAAGTG
                                                           426 GTTGGTATAGGGTTAATACTTACAGGAGCTTATTGGACATCAAGGATTTTGATAATAAT
                                                                                                                       486 GCTAAAAAAGCTGATTTTAAGTGGACTTGGGGTAAGGGAATGATGTTGGCAGGTGTGGTT
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFFWARE: ASCII Text
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Pred. No. 2.6e-06;
0; Mismatches 329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/830,228
FILING DATE: 24-Apr-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12764
FILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 98370PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 14:
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STRANDEDNESS: double
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STATE: Maryland
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Best Local Similarity
Matches 324; Conserv
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US-09-830-228-14
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APPLICANT: Gil Chol et. al.
TITLE OF INVENTON: Borrelia burgdorferi Polynucleotides and Sequences NUMBER OF SEQUENCES: 155
CORRESPONDENCE ADDRESS: 8383 AACGCAGACCTTAAAAAAAAACACTCGGCATTGCACTTGCGGGGCTTGAACCCAATTTTGAC 8442 7912 CICCATATATAAAATTTAAAAATTGTGCTAACATTCATTTATAAAAACTTAATTATTAGG 7971 ATAGGATCCTTTGTTCAAGGAGATTATATTGGTGGTGGTGCACTACTTGGCTCTCAAGTG 8211 8212 CTTGGAGGAATACTTATAATGGCTGGATACATGACCGGGGATATTGGATTCGTTACAGAA 8271 7972 AGGTAATATTAATATGAAAAATTTTCACATTAATATTAATTTTTAGTTTAACAATGCAA 8031 8032 ATCTTTGCACAAGAGAACTTGAAAAGGTGTTGGAGATATTGCAACCGTAATGAAATAT 8091 486 GCTAAAAAAGCTGATTTTAAGTGGACTTGGGGTAAGGGAATGATGTTGGCAGGTGTGGTT 545 TCTATTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAGGTTAAATTTAAATAGTTCCAA 131 132 AAGCCTTTTTTAAATTTCATTAATATGCTACCA-----TAATACCAGTTTAATAAAGGG 185 246 GCTCAAGATGATTCTAAAAGCACTTTTAATCTGGGAGCGGGAGAAAATTTTGGTTTAT 305 GAAACTAATAAGAAAGATTCTCTTGTACCATTTTTATTGAACCTTTTTTAGGGTTCGGG 365 ATAGGITCTTTTGCTCAAGGAGATATCCTTGGAGGTTCTCTTATTCTTGGATTTGATGCG 425 GTTGGTATAGGGTTAATACTTACAGGAGCTTATTTGGACATCAAGGATTTTGATAATAAT 485 AACAGGAAGCTGAAAAATAGTCTTAATATATAGCCTTGGGAGGATTTGAGCCTAGTTTTGAT 665 8272 AGCACAGCAACAGTAATAACCGGAGGAGTATTATCAGGAAT-----AGGAGGGCTC ACTATGGCTGTGACAAGATTGACAGAATTGTTCTTCCATTTACATTTGCTAATTAT GITITIATGAATAAGTTTTTAATTTTTATTTTGGTAATCTTTTGTGCTTTTTCTAGTTTT ZIP: 20850 COMPUTER READABLE FORM: MEDIUW TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 us-09-508-487-22.rnpm

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SEQUENCE CHARACTERISTICS
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                                   CORRESPONDENCE ADDRESS
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                                                                                                         STATE: Maryland
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Matches 333; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 GGCTGTGACAAGATTGACAGAAATTGTTCTTCCATTTACATTTGCTAATAATTATAACAG
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                                                                                                                                                                                                                                                            Length 7074;
                                                                                                                                                                                                                                                                                             0; Mismatches 308;
                                                                                                                                                                                                                                                            Score 82.2; DB 1;
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/09830228
GENERAL INFORMATION:
APPLICANT: Gil Choi et. al.
              NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 7074 base pairs
                                                                                                                                                                                                                                                           11.0%;
49.9%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           Best_Local Similarity 49.9
Matches 333; Conservative
                                                                                                                                                                        nucleic acid
EDNESS: double
                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATAAGC 3624
                                                                                                                                                                                        STRANDEDNESS:
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PCT-US98-12764-19
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                                                                                                                                                                                                                                                            Query Match
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TITLE OF INVENTION: Borrelia burgdorferi Polynucleotides and Sequences NUMBER OF SEQUENCES: 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAAGA---TAAGCTTGAAAAAAGTGTTGGAAGTATTGAAACCATTATGAAATATAAAAG 3278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3339 ATCCTTTGTCCAAGGAGATTATATTGGTGGTGGCGCAGTGCTTGGATCTCAGTTATTAGG 3398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3399 AGGAATACTITGCATAGCIGGAAATATICTIGGCCATACAGATGATGAAGAAGAGGAAC 3458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 AGATGATTCTAAAAGCACTTTTAATCTGGGAGCGGGAGAAAATTTTTGGTTTATGAAAC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 AAGCCTTTTTTAAATTTCATTAATATGCTACCA-TAATACCAGTTTAATAAAGGGGTTTT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATGAATAAGTITITAATITITATITIGGTAATCTITIGGGGTTTTTGTGCTTAGTTTTGCTCA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 TAATAAGAAAGATTCTCTTGTACCATTTTTATTGAACCTTTTTTAGGGTTCGGGATAGG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 ITCTTTTGCTCAAGGAGATATCCTTGGAGGTTCTCTTATTCTTGGATTTGATGCGGTTGG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATAGGGTTAATACTTACAGGAGCTTATTTGGACATCAAGGATTTTGATAATAATGCTAA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAGTTAAAATTTAAATAGT-TCCAA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAATAAAGATATTGTTAAAAGAATTGAAATTGCTAATTTTATGGTTAAATCAAGAAGCT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 7074;
                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.0%; Score 82.2; DB 32;
llarity 49.9%; Pred. No. 0.00011;
Conservative 0; Mismatches 308;
                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/830,228
FILING DATE: 24-Apr-2001
CLASSIFICATION - UNKNOWN>
PRIOR APPLICATION UNMBER: PCT/US98/12764
FILING DATE: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAME: BROCKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB370PCT
                                                                                                                                                                                                                                                                                                                                         COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                 Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                       STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 19:
                                                                                                 ADDRESSEE: Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 7074 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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Search completed: March 15, 2003, 09:01:10 Job time : 1473.7 secs

671 CATGGGC 677 || || || 3618 AATAAGC 3624 COLISON MANNE BOOK SIMI

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(without alignments)
10731.744 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                      501302 seqs, 350932545 residues
                                                                                nucleic search, using sw model
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                                                                                                                       Run on:
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inimum DB seq length: 0 aximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Maximum

Published_Applications_NA:* Database :

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/cgn2_6/ptodata/2/pubpna/MSO6_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/NSO7_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	-352-4584 Sequence 4584, Ap	S		S		S		S			US-09-790-988-1 Sequence 1, Appli					US-09-960-352-5301 Sequence 5301, Ap			Sequence
SUMMARIES	QI	US-09-960-352-4584	JS-09-938-842A-4130	US-09-790-988-1	JS-09-938-842A-5006	US-09-887-576-4	IS-09-938-842A-3659	US-09-960-352-4584	IS-09-754-853A-1	US-09-960-352-1452	096-60-sn	064-60-sn	0S-09-796	US-09-804	US-09-960-352-5558	IS-09-938-842A-4502	.096-60-sn	.096-60-SD	US-09-960-352-1496	US-09-960-352-3400
		10	9 9	10	<u>0</u>	10	6	10	<u>6</u>	10	10	10	01	10	70	D 6	10	70	10	10
	å Query Match Length DB	416	2000	640681	2000	2002	2000	416	127197	411	419	640681	2251	1058	431	2000	480	479	425	446
·	Query Match	6.4	6.3	6.0	5.7	5.7	5.7	5.6	5.6	5.6	5.5	5.5	5.5	5.5	5.4	5.4	5.4	5.3	5.3	5.3
	Score	55	54.2	51.8	49.2	49.2	48.8	48.4	48.2	48	47.4	47.4	47.2	47	46.6	46.6	46.2	46	45.8	45.4
_	Result No.	-	7	3	4	S	9	c 2	æ	ი ი	10	c 11	12	c 13	14	c 15	16	17	18	19

Sequence 4747, Ap Sequence 7, Appli Sequence 5087, Ap Sequence 5785, Ap	Sequence 4, Appli Sequence 2919, Ap Sequence 2919, Ap Sequence 1, Appli Sequence 1, Appli Sequence 1221, Ap	Sequence 2276, Ap Sequence 2276, Ap Sequence 1447, Ap Sequence 11234, A Sequence 11234, A Sequence 15, Appl	Sequence 10, Appl Sequence 35, Appl Sequence 13947, A Sequence 1739, Ap Sequence 1556, Ap	Sequence 4999, Ap Sequence 51, Appl Sequence 52, Appl Sequence 48, Appl
9 US-09-938-842A-4747 10 US-09-837-751-7 10 US-09-960-352-5087	0 00	10 US-09-770-663-9 10 US-09-954-456-2276 10 US-09-969-373-1447 10 US-09-960-352-6528 11 US-09-966-8528 9 US-09-966-880A-15 9 US-09-966-880A-7	9 US-09-966-880A-10 9 US-09-966-880A-35 10 US-09-960-352-13947 10 US-09-960-352-1739 10 US-09-764-869-1556	9 US-09-938-842A-4999 9 US-10-032-393-51 9 US-10-032-393-52 9 US-10-032-393-48
2000 5006 376 516	428 413 413 2846 4157 408	696 73308 371 414 419 2172 2818	6564 11204 299 385 26048	1367 9412 9412 9417
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45.2 45.2 44.8	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4444444 6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.	4 4 4 4 4 4 4 6 6 6 6 4 4 6 6 6 6	4 4 4 4 6 6 6 6 6
c 20 c 21 23 23	22 22 23 29 29	C C 30 C C 31 C 33 C 34 35	37 38 0 39 c 40	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Neappen
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AN
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: U5/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
ESEQ ID NO 4584
LENGTH: 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 TITAAIAAAGAGGITITITAIGAAIAAAITITIAAAITGITGITITGCIAGCCITITGIGIT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 TGGTCAAATCAAGAAGCTCTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAAGTTA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 AATTTGTAGAATTTTCGACAAATAAAGACATTATTAAAAGAATTGAAATTGCTAATTTTA 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB3057-016-Q1-K1-E11
US-09-960-352-4584
ALIGNMENTS
                                                                                                                            Sequence 4584, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION: APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
                                                                                                    US-09-960-352-4584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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Sequence 5006, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joe1

APPLICANT: And, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3

CURRENT APPLICANTION NUMBER: US/09/938,842A

CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 5379

SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212121 TTCATTTTTTAAAATATTAAAAAGAACTGTTTTTTAAAAACTTTTTTAGATGCATTAATT 212180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ATTGAAATTGCTAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAGCGAATTTCAAGT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 AATACTTTGAAAAAAGTTAAATTTTAAATAGTTTTAAAAACCTTTTTTAAATTTCATTAAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 AAAGACATTATTAAAAGAATTGAAATTGCTAATTTTATGGTCAAATCAAGAGCTCTATT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 AAAGCAAGGATTTAGAAGATTTAAATCTTTAAATTATTTTCATTAATAATAATTAA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 GGGAAGCGAATTTCAAGTAATACTTTGAAAAAGTTAAATTTAAATTTTAAAATTTTAAAAACCT 163
                                                                                                                                                                                                                                                                                                                                                                          2 ATTTTTCATTGGATCCCAGAATTTGTAGAATTTTCGACAATAAAGGACATTATAAAAGA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 640681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2000;
                                                                                                                                                                                                                                                                         Score 51.8; DB 10;
Pred. No. 2;
0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.7%; Score 49.2; DB 9; Best Local Similarity 47.4%; Pred. No. 3.5; Matches 147; Conservative 0; Mismatches 163;
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION WUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-5006
                                                                                                                                                                                                                                                                         Query Match 6.0%;
Best Local Similarity 50.6%;
Matches 125; Conservative
                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
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                                                                                                                          SEQ ID NO 1
LENGTH: 640681
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                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE PEFERENCE: SCRIP1300-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAAGTTAAATTTAAATAGTTTTAA 157
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Patent No. US20020127687A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYOKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                261 TITICIAGCITIGCICAAGCIGAIGATICIAAAAGCGCTTITAAITT 307
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Pred. No. 0.49;
0; Mismatches 188;
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4130
                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                     Sequence 4130, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4130
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Best Local Similarity 47.0%;
Matches 167; Conservative
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US-09-790-988-1
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GENERAL INFORMATION:
APPLICANT: Harper, Jeff
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   344 TAAGAAAGAT 353
                                    530 AATTAATGCT 539
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                                                                                          RESULT 6
US-09-938-842A-3659
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                                                                      351 ACGTTTAGTAAGAATATTTATTTAACAAAAAACTTTGTTTTAAATATTTGTTAACAA 410
                                                                                                                                          411 ATATGTTTATGCTAATTTTAAGGGATTGATTTGAAGTTTGTTAGGATTAAATTTGATTGA 470
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                                   164 TITITAAAITICATTAATATGTTACTATAATACCAGTTTTAATAAAGAGGTTTTTATGAA
                                                                                                       TGATTCTAAAAGCGCTTTTAATTTGGGAGCGGGAGAAAAACTTTTAGCTTATGAAACTAG
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TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1360.001US1
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Best Local Similarity 47.4%; Pred. No. 3.5;
Matches 147; Conservative 0; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR PLIING DATE: 2000-06-23
PRIOR PLIING DATE: 2000-06-23
PRIOR PLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09887576
Patent No. US20020144047A1
GENERAL INFORMATION:
APPLICANT: Budworth, P.
APPLICANT: Brown, D.
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US-09-887-576-4
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Chang, H.
Zhu, T.
Han, B.
Wang, X.
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Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US 60/227, 866
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR APPLICATION NUMBER: US 60/24, 647
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AN TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 TAAGAAAGATCCTATTGTGCCATTTTTATTGA 375
Sequence 3659, Application US/09938842A Patent No. US20020160378A1
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Patent No. US20020137139A1
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Best Local Similarity 46.7%;
Matches 155; Conservative
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
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APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REPERBUCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
PRIOR TELLIG DATE: 2001-01-05
PRIOR FILLING DATE: 2000-01-07
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                                                                                                                                                                                                                                                                                                                                            TCAAGTAATACTTTGAAAAAGTTAAATTTAAATAGTTTTAAAAAACCTTTTTAAAATTTC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 TGGTCAAATCAAGAAGCTCTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAAGTTA 140
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                                                                                                                                                                                              Length 416;
                                                                                                                                                                                                                               Indels
                                                                                         TYPE: DNA
CRGANISM: Bos taurus
CTHER INFORMATION: Clone ID: 20-LIB3057-016-Q1-K1-E11
US-09-960-352-4584
                                                                                                                                                                                        Score 48.4; DB 10;
Pred. No. 4.1;
0; Mismatches 176;
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45.8%; Pred. No. 7.3;
Live 0; Mismatches 198;
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US-09-754-853A-1
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 4584
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                                                                                                                                                                                        Query Match 5.6%;
Best Local Similarity 46.7%;
Matches 154; Conservative
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Best Local Similarity
Matches 167; Conserv
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US-09-754-853A-1
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Sequence 1451, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wealey C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
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                                                                                                        AATTTAAATAGTTTTTAAAAACCTTTTTTAAATTTCATTAATATGTTACTATAATACCAGT
                                                                                                                                                                                                                                              TITAATAAAGAGGITITITATGAATAAATTTTTAATTGTTGTTTTGCTAGCCTTTTGTGTT
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46.0%; Pred. No. 4.8;
Live 0; Mismatches 190; Indels
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ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 62-LIB3058-002-Q1-K1-H6
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| 55795 TATTT 55799
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Db 625163 TATAAATTTGFATAATAGATAGCCTTTTTAGAAAAAAGGAGAATAACTTTGGATTGATAT 625104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Carrawy, wherein T APPLICANT: Carrawy, bendied T APPLICANT: Carrawy, bendied T APPLICANT: Smeltzer, Richard H TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms; FILE REFERENCE: 50617/c-3532.0 CURRENT APPLICATION NUMBER: US/09/796,256A CURRENT FILING DATE: 2001-02-28 PRIOR APPLICATION NUMBER: US/09/3381 PRIOR PLILNG DATE: 1996-12-16 PRIOR FILING DATE: 1997-12-16 NUMBER OF SEQ ID NOS: 11 SEQ ID NO 11 SEQ ID NO 11 SEQ ID NO 11 LENTH: 2251
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                  Indels
                101;
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  Pred. No. 11;
0; Mismatches
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                                                                                                                                                                                                                                                                                                       AAAGAGGTTTTTATGAATAAATTTTTAAT 235
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Patent No. US20020078477A1
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Local Similarity 51.7%;
hes 108; Conservative
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APPLICANT: Chiang, Vincent L
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ORGANISM: Pinus taeda
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US-09-796-256A-11
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  Best Loc
Matches
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                                                           Sequence 11234, Application US/09960352
Patent No. US2002013713941
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagapan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 13112
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Patent No. US20020127687A1
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 48-LIB3058-052-Q1-K1-D8
[S-09-960-352-11234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 136;
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Pred. No. 6.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUCKRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTATTTTTTAAATATATATTTA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.5%;
Best Local Similarity 48.7%;
Matches 129; Conservative
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US-09-790-988-1/c
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Score 46.6; DB 10; Length 431;
Pred. No. 8.4;
0; Mismatches 184; Indels 0
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 24-LIB3057-024-Q1-K1-F7
US-09-960-352-5558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 TTGGGGGTTTTCTTATTCTTGGATTTGATGCAGTTGGTATA 464
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                                                                                              Sequence 5558, Application US/09960352 Patent No. US20020137139A1
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Best Local Similarity 46.0%;
Matches 157; Conservative
                                                                                                                                        GENERAL INFORMATION:
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US-09-938-842A-4502/c
                                                         RESULT 14
US-09-960-352-5558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTAGCTTTGCTCAAGCTGATGATTCTAAAAGCGCTTTTAATTTGGGAGCGGGAGAAAAC 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         963, 965, 966, 967, 968, 969, 991, 994, 996, 998, 999, 1001, 1020, 1021, 1023, 1024, 1025, 1042, 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          732 TGNAAAATNTTAGNGTTATTGGAAANCAAANGNGAAAATATTTTCNAAGAAGNNAAAGGG 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAATCAAGAAGCTCTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAAGTTAAATT 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 TAAATAGTTTTAAAAACCTTTTTTAAATTTCATTAATATGTTACTATAATACCAGTTTTA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   612 ITAAANCAACTGATGGCCACGTTTTANATANTCTTGATGTATATGTTGAATTACATGTCA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITIAGCITATGAAACTAGTAAGAAGATCCTATTGTGCCATTTTTATTGAACCTTTTTT 384
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871, 872,
900, 903,
929
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                                APPLICANT: Corey, Michael J.
TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THE SAME AND METHODS FOR SCREENING FOR (TITLE OF INVENTION: MODULATING THE SAME
FILE REFERENCE: 130001.406
CURRENT APPLICATION NUMBER: US/09/804,682
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 ATAAAGAGGTTTTTAFGAATAAATTTTTAATTGTTGTTTTGCTAGCCTTTTGTGTTTTTT
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863,
893,
921,
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862,
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919,
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861,
891,
916,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 930, 931, 950, 951, 954, 957,
LOCATION: 1006, 1008, 1009, 1010, 1017,
LOCATION: 1027, 1031, 1034, 1035, 1039,
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: 816, 819, 81, 82, 855, 856, E
LOCATION: 850, 851, 853, 855, 856, E
LOCATION: 973, 879, 881, 883, 886, E
LOCATION: 904, 905, 906, 909, 913, OTHER INFORMATION: n = A,T,C or G
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US-09-804-682-30
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Best Local Similarity 42.6'
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 7, 9, 88, 462, 5
LOCATION: 687, 700, 702, 7
LOCATION: 785, 761, 764, 7
LOCATION: 785, 787, 788, 7
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LOCATION: 1046, 1058
                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                SEQ ID NO 30
LENGTH: 1058
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APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: WUSCLE AND END DECCURENT APPLICATION WURBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
SEQ ID NOS: 15112
SEQ ID NO 5558
LENGTH: 431
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Sequence 4502, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION UNMERR: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 TGCTAGCCTTTTGTGTTTTTTTTTTGTGCTTTGCTGAGCTGATGATTCTAAAAGCGCTTTTA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 ATTTGGGAGCGGGAGAAAACTTTTAGCTTATGAAACTAGTAAGAAGATCCTATTGTGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 CATITITATIGAACCTITITITAGGGTTTGGAATAGGTTCTTTTGCTCAAGGAGATATTC 423
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                                                                                                                                                                                                               163 TTTTTAAAATTTCATTAATATGTTACTATAATACCAGTTTTAATAAAGAGGTTTTTATGA 222
                                                                                                                                                           43 TAAAGACATTATTAAAAGAATTGAAATTGCTAATTTTATGGTCAAATCAAGAAGCTCTAT 102
                                                                                                                                     Gaps
                                                                                                         Length 2000;
                                                                                                        Query Match 5.4%; Score 46.6; DB 9; Length 20
Best Local Similarity 50.7%; Pred. No. 9.6;
Matches 112; Conservative 0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                         ; PRIOR FILING DATE: 2001-06-22; NUBBER OF SEQ ID NOS: 5379; SEQ ID NO 4502; LENGTH: 2000; TYPE: DNA ORGANISM: A TABLIDOPSIS thallana US-09-938-842A-4502
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Search completed: March 15, 2003, 14:21:27 Job time: 525.376 secs

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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 14:19:56; Search time 31 Seconds
(without alignments)
765.116 Million cell updates/sec
Title: US-09-508-487-21
Perfect score: 904
Sequence: 1 MNKFLIVVLLAFCVFSSFAQ......DINMGQASALGFELSFKKSY 178
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Total number of hits satisfying chosen parameters:

908470 segs, 133250620 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

908470

inimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

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sec	DS1	DS1	DS1	DS1	DS1	DS1	051	DS1	S S	IDS	ä	ñ	ips	ips	ă	ID:	ñ	SIDS1	SIDS1,	IDS	SIDS1	IDS	IDS
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Borrelia afzelii A	Borrelia qarinii I	B. burgdorferi ant	Borrelia buradorfe	B. burgdorferi ant	pll protein sequen	Borrelia burgdorfe	Corynebacterium ql	C qlutamicum prote	B. burgdorferi ant
SUMMARIES	ΩI	AAY04279	AAY04280	AAY19808	AAY04278	AAY19809	AAY04282	AAY04281	AAB76781	AAG93096	AAY19965
	DB	20	20	20	20	20	20	20	22	22	20
	% Query Match Length DB	178	177	179	179	158	95	25	345	417	479
	å Query Match	100.0	87.0	85.1	85.1	76.1	17.7	13.7	10.7	10.7	10.6
	Score	904	786.5	769.5	769.5	687.5	160	124	97	97	95.5
	Result No.	1	7	m	₹	S	9	7	80	σ	10

B. burgdorferi ant Listeria monocytog	Streptococcus pneu	Streptococcus pneu	H. pylori GHPO 132	Human polypeptide	Botulism toxin hea	Botulism toxin hea	Botulinum neurotox	Recombinant botuli	A manganese supero	A manganese supero	Recombinant botuli	Clostridium botuli	Helicobacter polyp	Micromonospora eve	E. coli cellular p	Salmonella typhi c	E. coli growth and	Rhizobium DMP. Rh	Lactococcus lactis	Propionibacterium	Lactococcus lactis	Staphylococcus aur	Staphylococcus aur	Helicobacter pylor	Listeria monocytog	Listeria monocytog	Arabidopsis thalia	A. thallana inorga	Arabidopsis thalia	Herbicidally activ	Herbicidally activ	Tomato phosphate t	Drosophila melanog
ABB50049	AAY81595	AAU37748	AAW98808	AAM41896	AAB04097	AAB04082	ABG69077	AAW56018	AAY93308	AAY93311	AAW56017	AAW68392	AAW71476	AAU04855	AAU34477	AAU38487	AAG98862	AAR79372	ABB54849	AAU58659	ABB54275	AAU34379	AAU37465	AAU35869	ABB47392	ABB49960	AAW32302	AAW36137	AAW46748	ABB92038	ABB92665	₹	ABB66943
20	21	22	19	22	22	22	23	19	21	21	19	19	19	22	22	22	22	16	23	22	23	22	22	22	23	23	18	18	19	23	23	19	22
504 364	572	650	215	259	413	848	852	828	1070	1095	1169	1291	302	251	663	663	. 663	444	490	571	635	411	432	206	382	463	534	534	534	534	535	538	180
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95.5	83.5	83.5	82.5	81.5	81.5	81.5	81.5	81.5	81.5	81.5	81.5	81.5	81	79	78.5	78.5	78.5	77.5	77	76.5	76.5	97	92	75.5	75.5	75.5	75	75	75	75	75	75	74.5
11	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	.30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

dard; Prote (first ent. lii ACAI pa antigen; 8 111. 97US-0059 97US-0059 97US-0059 97US-180] 227/18. 1999. from Borrel	AAY04279 AAY04279 XX AAY04279; XX AAY04279; XX XX XX XX XX XX XX XX XX	ein; 178 AA. .y)	Borrelia afzelii ACAI protein. Borrelia; P13 antigen; spirochaete; vaccine; infection; diagnosis.	424. 9036. 1041.		WPI; 1999-215027/18. N-PSDB; AAX30099. Nucleic acid from Borrelia burgdorferi encoding virulence associated protein Pl3
	LT 1 4279 AAY04279 stance AAX04279; 17-JUN-1999 Borrelia afze Borrelia afze WO9912960-A2. 18-MAR-1999. 04-SEP-1997; 16-SEP-1997; 16-SEP-1997; (SYMB-) SYMBIG Bergstroem S; WPI; 1999-2156 WPI; 1999-2156 NPI; 1999-2156	dard; Prote (first ent	lii ACAI pr antigen; s	 98WO-IB01424. 97US-0059036. 97DK-0001041.	COM AB.	027/18. 099. from Borrel

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present sequence represents a Borrelia garinii IP90 protein. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY19808 standard; Protein; 179 AA
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97US-0050359.
97US-0053344.
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N-PSDB; AAX61505.
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                                                                          The present sequence represents a Borrelia afzelii ACAI protein. The present invention describes an isolated nucleic caid (1) that: (i) crocodes a polypeptide fragment (II) immunologically reactive with accodes a polypeptide fragment (II) immunologically reactive with cabbit polyclonal antibody raised against a 13 kDa polypeptide of Borrelia burgdorferi B313, but not reactive with most proteins from ther spirochaetes; and/or (ii) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most other spirochaetes; (I), (II) and transformed cells are useful in caccines to protect against infection by B. burgdorferi sensulation (I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The I3 KD protein is involved in virulence and is highly conserved within B. burgdorferi sensulato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis, compared with use of whole bacteria as antigen.
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100.0%; Pred. No. 2.3e-92;
ive 0; Mismatches 0;
Claim 31; Page 111-112; 118pp; English.
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97DK-0001041.
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78; Conservative
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N-PSDB; AAX30100.
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10-SEP-1997;
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Best Local Simi
Matches 178;
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present invention describes an isolated nucleic acid (1) that: (i) encodes a polypeptide fragment (11) immunologically reactive with encodes a polypeptide fragment (11) immunologically reactive with crabbit polyclonal antibody raised against a 13 kba polypeptide of Borrella burgdorferi Bill, but not reactive with most proteins from other spirochaetes; and/or (ii) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most other spirochaetes. (1), (II) and transformed cells are useful in vaccines to protect against infection by B. burgdorferi sensu lato. (I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (1) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi sensu lato, but is absent from other Borrellas species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis, 61 GSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAVT 120 1 MNKFLIVVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKKDPIVPFLLNLFLGFGI Antigenic protein; vaccine; Lyme disease; infection; detection. Length 177; 16; Indels 87.0%; Score 786.5; DB 20; 86.5%; Pred. No. 2.6e-79; compared with use of whole bacteria as antiqen. Lathigra R; 7; Mismatches B. burgdorferi antigenic protein, f933.aa.

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other spirochaetes. (I), (II) and transformed cells are useful in vaccines to protect against infection by B. burgdorferi sensu lato.
(I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi sensu lato, but is absent from other Borrealia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis, compared with use of whole bacteria as antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY19809;
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                         This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in mamans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 IGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASALGFELSFKKSY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNKFLIVVLLAFCVFSSFAQADDSKS-AFNLGAGEKLLAYETSKKDPIVPFLLNLFLGFG 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrella; P13 antigen; spirochaete; vaccine; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                        85.1%; Score 769.5; DB 20; Length 179; 84.9%; Pred. No. 2e-77; 1ve 10; Mismatches 16; Indels 1;
            Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 31; Page 108-109; 118pp; English.
                                                                         275pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borrelia burgdorferi B31 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY04278 standard; Protein; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-IB01424.
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97DK-0001041.
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                                                                      Page 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                    179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX30098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 152;
               caused by
                                                                      Claim 12;
                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY04278
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                                                                                                                                            60 IGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAV 119
                                                Gaps
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                                                                                                                                                                               120 TMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASALGFELSFKKSY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to develop
diseases
                                                                                      Antigenic protein; vaccine; Lyme disease; infection; detection.
                                                ä
                    Length 179;
                                                Indels
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                      DB 20;
                     85.1%; Score 769.5; DB
84.9%; Pred. No. 2e-77;
iive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lathigra R;
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                                                                                                                                                                                                                                                                        AAY19809 standard; Protein; 158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 73; 275pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                                                                          (first entry)
                                     Local Similarity 04.7
les 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-189980/16.
                                    Similarity
179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX61506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                WO9859071-A1.
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                                                                                                                                                                                                                                                                                                                          19-JUL-1999
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compared with use of whole bacteria as antigen. The present sequence represents a pl1 protein sequence from a best hit search.

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The present invention describes an isolated nucleic acid (I) that: (i) encodes a polypeptide fragment (II) immunologically reactive with rabbit polychonal antibody raised against a 13 kba polypeptide of crabbit polychonal antibody raised against a 13 kba polypeptide of crabbit burgdorferi B313, but not reactive with most proteins from cother spirochaetes; and/or (ii) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most cher spirochaetes. (I), (II) and transformed cells are useful in vaccines to protect against infection by B. burgdorferi sensu lato.

(I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi sensu lato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis,
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humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                               GIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTFANSYN 140
                                                                                                                                            Gaps
                                                                                                                                                                          22 DDSKS-AFNLGAGEKLLAYETSKKDPIVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid from Borrelia burgdorferi encoding virulence associated
                                                                                                                                                                                            Borrelia; Pl3 antigen; spirochaete; vaccine; infection; diagnosis.
                                                                                                        DB 20; Length 158;
                                                                                                                                                                                                                                                                                                              RKLKNSLNIAFGGFEPSFDINMGQASALGFELSFKKSY 178
                                                                                                                                                                                                                                                                                                                               76.1%; Score 687.5; DB 285.4%; Pred. No. 2.3e-68;
                                                                                                                                          10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 8; Page 118; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                                                                                                                                                                              AAY04282 standard; Protein; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0059036.
97DK-0001041.
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                                                                                                                       Best Local Similarity 85.45
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pll protein sequence
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N-PSDB; AAX30115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYMB-) SYMBICOM AB.
                                                                     158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bergstroem S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09912960-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-1999
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                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY04282;
                                                                                                        Query Match
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The present sequence represents a Borrelia burgdorferi B313 N-terminal peptide. The present invention describes an isolated nucleic acid (I) that: (i) encodes a polypeptide fragment (II) immunologically reactive with rabbit polyclonal antibody raised against a 13 kDa polypeptide of Borrelia burgdorferi B313, but not reactive with most proteins from other spirochaetes; and/or (ii) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most other spirochaetes (I), (II) and transformed cells are useful in vaccines to protect against infection by B. burgdorferi sensu lato. (I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II): The I3 kD protein is involved in virulence and is highly conserved within B. burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sensu lato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis, compared with use of whole bacteria as antigen.
                                                                                                                Gaps
                                                                                                                                                                            1 MKKIFTLILIFGLTIBIFA-TKDTQNRIEKGI-ESFNKYDKEKKNPIGPFLLNLFLPFGI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid from Borrelia burgdorferi encoding virulence associated
                                                                                                                                             1 MNKFLIVVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKKDPIVPFLLNLFLGFGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia; P13 antigen; spirochaete; vaccine; infection; diagnosis.
                                                                                                                2
                                                                                Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25;
                                                            Score 160; DB 20,
""nd. No. 5e-10;
"na 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.7%; Score 124; DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi B313 N-terminal peptide.
                                                                                                 ; Pred. No. 5e-1
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 49; 118pp; English.
                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                         AAY04281 standard; peptide; 25
                                                                                                                                                                                                                             59 GSFVQGDYIGGGSVLGFNLLG 79
                                                                                                                                                                                                            61 GSFAQGDILGGFLILGFDAVG 81
                                                                              17.78;
44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-IB01424.
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                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                              36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi.
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                                                                                               Similarity
                                               95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bergstroem S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9912960-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein P13
                                                                                                                                                                                                                                                                                                                                                         AAY04281;
                                                Sequence
                                                                              Query Match
Best Local $
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AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.

AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
                                    Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation -
                                                                                                                                                                                                                                                                                                                                                                                                                                         PWKLFK-----NMLPAYFTALGTSSSAATIPVT----YQQTLKNDVDVNVAGFVVPLCA 210
                                                                                                                                                                                                                                                                                                                                                                         48 VP-FLLNLFLGFGIGSFAQGDIL-----GGFLILGFDAVGIGLILTGAYLDIKALDKNA 100
                                                                                                                                                                                                                                                                                                                                                                                                 LPLFIFGIFLGMGM----NGGLLEIMSAFGKVLILA--VVGTLLFLAIQFIIAGAVSKKN 160
                                                                                                                                                                                                                                                                                                                                                                                                                        PKAAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEP---- 156
                                                                                                                                                                                                                                                                                                                                                   63 MTALLLAFC-------LGLGMAVIKSDTLFKVTRELERVVMKTITAFVIPL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                     80;
                                                                                                                                                                                                                                                                          10.7%; Score 97; DB 22; Length 345; 23.1%; Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ochiai K,
                                                                                                                                                                                                                                                                                                   62; Indels
                                                                                                                                                                                                                                                                                                                            5 LIVVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKK-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C glutamicum protein fragment SEQ ID NO: 6850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- SFDINMGQASALGFEL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 TIHLAGSMMKIGLFTFAVVFMYDMEVGVGLSIGFLL 246
                                                                                                                                                                                                                                                                                                   24; Mismatches
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w Ozaki A;
                                                                                            Claim 20; Page 925-926; 1119pp; English.
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Senoh A, Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG93096 standard; Protein; 417
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                   50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organic acid synthesis.
                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                     345 AA;
           N-PSDB; AAF68014
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07-APR-2000;
03-AUG-2000;
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Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-2001
                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                 107
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                                                                                                                                                                                                                          Corynebacterium glutamicum; brevibacterium lactofermentum; MCT; membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation;
                        Gaps
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                        ö
                        Indels
                                                                                                                                                                                                     Corynebacterium glutamicum MCT protein SEQ ID NO:544.
9.5e-07;
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                        Mismatches
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9
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                                              65
                                                          AAB76781 standard; Protein; 345
                       1;
                                              TSKKDPIVPFLLNLFLGFGIGSFAQ
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990E-1032124.
990E-1032125.
990E-1032128.
990E-1032180.
           96.0%;
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99DE-1032212.
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                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum.
                                                                                                                                                                             (first entry)
         Local Similarity 96.0 ses 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99DE-10407
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                                                                                                                                                                             11-APR-2001
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03-SEP-1999
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                                                                                                                                                     AAB76781;
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-JUL-1
-JUL-1
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- 40L-1
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                      Matches
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This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||::| ||||
93 IVIILPFCVFLAIFFCLIWSSF---DDLIASLGLFVFRFEYFGSFLYGFLNRLLIPLGLH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 AVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTFANS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LINLF----LGFGIGSFAQG--DILGGF-LILGFD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 IVVLLAFCVF----SSFAQADDSKSAFNLGA-----GEKLLAYETSKKDPI--- 47
                                                                                                                             products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigenic protein; vaccine; Lyme disease; infection; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                            10.6%; Score 95.5; DB 20; Length 479; 25.5%; Pred. No. 0.056; Live 25; Mismatches 67; Indels 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 YNRKLKNSLNIAFGGF----EPSFDINMGQASALGF 170
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                                         Hanson MS, Lathigra R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lathigra R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B. burgdorferi antigenic protein, f843.aa.
                                                                                                                                                                                                     Claim 12; Page 139-140; 275pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY19964 standard; Protein; 504
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97US-0053344.
97US-0053377.
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   (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi
                                       Erwin AL,
                                                                        WPI; 1999-189980/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                          479 AA;
                                                                                             N-PSDB; AAX61662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 ----VPF-
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                       Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                            The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VP-FLINLFLGFGIGSFAQGDIL-----GGFLILGFDAVGIGLILFGAYLDIKALDKNA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 LPLFIFGIFLGMGM----NGGLLEIMSAFGKVLILA--VVGTLLFLAIQFIIAGAVSKKN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 PWKLFK-----NMLPAYFTALGTSSSAATIPVT----YQQTLKNDVDVNVAGFVVPLCA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTALLLAFC-------LGLGMAVIKSDTLFKVTRELERVVMKTITAFVIPL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKAAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigenic protein; vaccine; Lyme disease; infection; detection
                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.7%; Score 97; DB 22; Length 417; 23.1%; Pred. No. 0.032; ive 24; Mismatches 62; Indels
                                                                                                                                              Claim 17; SEQ ID NO: 6850; 246pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIVVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SFDINMGQASALGFEL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 TIHLAGSMMKIGLFTFAVVFMYDMEVGVGLSIGFLL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.1%; Preu. ....

 B. burgdorferi antigenic protein, t843.aa.

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97US-0050359.
97US-0053344.
97US-0053377.
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Matches 50; Conservative
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2001-376931/40
                                                                                                                                                                                                                                                                                                                                                                                                                                             417 AA;
 WPI; 2001-376931,
N-PSDB; AAH68315.
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                                                                                                                                                                                                                                                                                    12;
                                                                                                                         This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fsihi H, Dehoux P;
Kunst F, Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                  79 AVGIGLILIGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTFANS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                    235 LPGAAL---GVYKGIVHEDKNKVAA------LLFSGALTAFLTGITE---PLEFLFI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amend A;
                                                                                                                                                                                                                                                                                                                                                                                        175 SILSFPFEFTSLGGVEIVNGDTVRGLKNIFYAQLLDPSLGKFSSGFAKISSGFYLSIMFG 234
                                                                                                                                                                                                                                                                                                                                      118 IVIILPFCVFLAIFFCLIWSSF---DDLIASLGLFVFRFEYFGSFLYGFLNRLLPLGLH 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Clarbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                            6 IVVLLAFCVF-----SSFAQADDSKSAFNLGA-----GEKLLAYETSKKDPI--- 47
                                                                                                                                                                                                                                                                                                                                                               48 ----VPF-----LILGFF-LILGFF----LGFGIGSFAQG--DILGGF-LILGFD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                              New isolated Borrella burgdorferi nucleic acids – used to developroducts for the diagnosis, prevention and treatment of diseases caused by Borrella, particularly Lyme disease
                                                                                                                                                                                                                                                                                   :69
                                                                                                                                                                                                                                                            Length 504;
                                                                                                                                                                                                                                                                                67; Indels
                                                                                                                                                                                                                                                         10.6%; Score 95.5; DB 20; 25.5%; Pred. No. 0.059; ive 25; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 YNRKLKNSLNIAFGGF----EPSFDINMGQASALGF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 FTAPLLYFVHAAYSGFALLLANFFNVTIGNSFSTGF 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria monocytogenes protein #2753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB50049 standard; Protein; 364 AA
                                                                                                   Claim 12; Page 139; 275pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2000; 2000FR-0004629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-2002 (first entry)
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 25.5%
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INSP ) INST PASTEUR.
          WPI; 1999-189980/16.
                                                                                                                                                                                                                                 504 AA;
                        N-PSDB; AAX61661
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                                                                                                                                                                                                                                  Sequence
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ABB50049
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The present invention relates to the genome sequence of Listeria

monocytogenes BCD-e (see ABA03041). The genome sequence and fragments of
it are useful for selecting probes and primers for detecting genes in L.
monocytogenes and related organisms, and for studying genetic
monocytogenes and related organisms, and for studying genetic
monocytogenes and other genomes. The present invention proteins
concord by the genome sequence of the present invention. Proteins
expressed from the genome sequence of the present invention. Proteins
cartibodies, identification of L. monocytogenes and related organisms, and
for biosynthesis and biodegradation, especially biosynthesis of vitamin

B12. The genome sequence and proteins encoded by it are also useful for
selecting compounds that regulate gene expression and cell replication
and modulate L. monocytogenes-related diseases. In addition, the genome
sequence and proteins encoded by it are useful in pharmaceutical and
vaccines compositions for the treatment or prevention of infections by L.
cc monocytogenes and related organisms.

Cnocytogenes and related organisms.
Cnocytogenes and related organisms.
Cnocytogenes and electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 IAYSIADRPGIAPGLIMGLIANSIGAGFLGGMLGGYL-----VGYFVLILVKYLKV--- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 DKNAPKAAFKWTWGKGMM-----LAGAVTMAVTRLTEIIIPFTFA----NSYNRKLKNS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 ----PK-----WAQGLMPMMIIPLISSLVVGLLMYFVVGVPIVWATEAMTSFLQGMQGS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 LAYETSKKDPIVPFLLENLFLGFGIGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKAL 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis;
                                                                                                                                           Genomic sequence for Listeria monocytogenes, useful e.g. for tree and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae type 4 protein sequence #95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.4%; Score 85; DB 23
Local Similarity 23.5%; Pred. No. 0.58;
tes 32; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                         Claim 6; SEQ ID No 2754; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY81595 standard; Protein; 572 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-GB02451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 MRFVFGAVLGAMAAFD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae.
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                                                                            WPI; 2002-010914/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 AA;
Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200006737-A2
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19-MAR-1999;
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    Rose M,
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99US-0125164.

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H. pylori GHPO 1325 protein.
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            (ELIT-) ELITRA PHARM INC
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Best Local Similarity
Matches 39; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori.
                                                                       WPI; 2001-611495/70.
                                                                                  N-PSDB; AAS55607
                                    Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1998;
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                                                                                                                                          AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful as immunogens diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the exemplification of the present invention.
                                                                     New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                       341 AGALVLAIKKYVKVPRSLEGAKSILLPLLGTILTGFVMLAVNIPMAAINTAMNDFLGG- 399
                                                                                                                                                                                                                                                                                                                                                                                                                                   73 LILGFDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLA----- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                32 AGEKLLAYETSKKDP-----IVPFLLNLFLGF------GIGSFAQGDILGGF 72
                                                                                                                                                                                                                                                                                                                                     9.2%; Score 83.5; DB 21; Length 572; ilarity 25.3%; Pred. No. 1.5; Conservative 22; Mismatches 54; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae cellular proliferation protein #177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 --VTRLTEIIIPFTFANSYNRKLKNS--LNIAFG 152
                                                                                                                      Claim 1; Page 81; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU37748 standard; Protein; 650
(MICR-) MICROBIAL TECHNICS LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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2000US-206848P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                        Hansbro PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae
                                               WPI; 2000-195300/17
                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 39; Conserv
                                                                                                                                                                                                                                                                                                                572 AA;
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                       Gilbert CFG,
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16-FEB-2001;
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23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-2002
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                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                             Matches
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prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes, their use in the discovery of novel antibiotics, the essential genes themselves and the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coll, Staphylococcus aureus, Salmonella typhi, Klabsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets of or antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Control of the printed specification, but was obtained in electronic for the printed specification, but was obtained in electronic for the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 AGALVLAIKKYVKVPRSLEGAKSILLEPLIGTILTGFVMLAVNIPMAAINTAMNDFLGG- 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 LILGFDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLA-----GAVTMA---- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antisense inhibitors of genes essential to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 650;
Trawick JD,
                                                                                                                                                                                                                                                                    New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.2%; Score 83.5; Dilarity 25.3%; Pred. No. 1.8; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --VTRLTEIIIPFTFANSYNRKLKNS--LNIAFG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : :::|| | 534 GWVPPLAIFVATLLFKDKFTKEERNSGLTNIIMG 567
                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Seq ID No 13341; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
Ohlsen KL, Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW98808 standard; Protein; 215 AA.
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97US-0902615. 97US-0833457. 97US-0881227.

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Al-Garawi A, Kleanthous H, Miller C, Oomen RP,
                          (HUMA-) HUMAN GENOME SCI INC.
(INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
                                                      WPI; 1998-542293/46.
                                                            N-PSDB; AAX14527.
    29-JUL-1997;
01-APR-1997;
24-JUN-1997;
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Tomb J;

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This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis.
New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases
                                                                                                                                                                                                Claim 8; Page 1770-1771; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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65; Gaps 9.1%; Score 82.5; DB 19; Length 215; 23.0%; Pred. No. 0.57; ative 18; Mismatches 41; Indels 65 Query Match 9.1% Best Local Similarity 23.0% Matches 37; Conservative

9 ----ETS 42 38 IVMVLMAFCKIVSYEDIIKNKSAFNIFLLLGSLLTMAGGLKNVGFLNFIGNAAONFLEHA 97 5 LIVVLLAFCVFSSFAQADDSKSAFN------LGAGEKLLAY-----82 IGLILT------GAYLDIKALDKNAPKAAFKWTWG 110 q ò a õ ò

Search completed: March 14, 2003, 14:24:24 Job time : 33 secs

----WKWG 188

158 IMGILTPYGTGPSTIYYGSGYIQSKDF--

Also PACK BLANK IUSPIO,

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

 protein search, using sw model OM protein March 14, 2003, 14:22:16; Search time 12.3333 Seconds Run on:

(without alignments) 1387.454 Million cell updates/sec

US-09-508-487-21

1 MNKFLIVVLLAFCVFSSFAQ......DINMGQASALGFELSFKKSY 178 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

PIR_73:* Database

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	hypothetical proteconserved hypothet conserved hypothet conserved hypothet conserved hypothet probable sugar-prophosphorable c4 dicarb hypothetical prote NADH2 dehydrogenas hypothetical prote PTS system, fructo PTS system, fructo PTS system, fructo pTS system, fructo pTS system, fructo pTS system, fructo pTS system, fructo pTS system, fructo pTS system, fructo pTS system, fructo pTS system, fructo pTS system, fructo pTS system, fructo pTS system, fructo pTS system, fructo pTS system, fructo pTS system, fructo pTS system promease cytosine permease cytosine permease cytosine permease cytosine permease cytosine protein - tap gontoxilysin (EC 3 hypothetical prote conserved hypothet undecaprenyl-phosp D-nopaline dehydro
н	B70104 A70207 F70243 G70239 D70114 P7064 F75346 G98325 A62957 S7112 A61341 A61341 A71341 A71341 A71341 D97969 S75212 B83885 A45620 S75212 B83885 A45620 S75212 B7538 A76346 S7638 A7638 A7638 S7638 A7638 S7638 B6959 B6959 B6959 B6959
Length DB	170 171 170 170 170 170 170 170 170 170
å Query Match]	82 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Score	2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Result No.	100 8 8 7 9 7 8 8 7 9 8 8 7 9 8 8 7 9 8 8 7 9 8 8 7 9 8 8 7 9 9 8 8 7 9 9 8 8 7 9 9 8 8 7 9 9 8 8 7 9 9 8 8 7 9 9 8 8 7 9 9 8 7 9 9 8 7 9 9 8 7 9 9 9 8 7 9 9 9 9

N-heparan sulfate	conserved hypothet	cytochrome d ubiqu	ATP dependent heli	chloramphenicol re	CmlA protein - Pse	hypothetical prote	hypothetical prote	probable membrane	C4-dicarboxylate t	bo-type ubiquinol	cytochrome o ubiqu	cytochrome o ubiqu	bo-type ubiquinol	non-proteolytic bo	probable holocytoc
A42855	H72250	S75272	AD1457	A47033	JQ1201	E83723	T02512	AB0276	D83498	A85540	E90689	AE0557	B42226	140631	D69597
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882	183	336	779	419	419	429	539	372	436	663	663	663	663	1291	235
8.9	8.8	8.8	8.8	8.8	8.8	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.6
80.5	80	80	80	79.5	79.5	79	79	78.5	78.5	78.5	78.5	78.5	78.5	78.5	78
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	Lyme
	1
•	BB0034
	protein
1	stical
RESULT B70104	hypothetical

e disease spirochete

C; Species: Borrella broofferi (Lyme disease spirochete)
C; Species: Borrella broofferi (Lyme disease spirochete)
C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 17-Mar-2000
C; Accession: B70104
R; Fraser. C. M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; W son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; V son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hatch, B natura 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID: 98065943; PMID: 9403685
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: CNA
A;

3 > ₪

GB:AE000783; NID:g2687907; PIDN:AAC66426.1; PID:g26

1; Gaps Length 179; Indels Query Match 85.1%; Score 769.5; DB 2; Best Local Similarity 84.9%; Pred. No. 2.8e-63; Matches 152; Conservative 10; Mismatches 16;

1;

QQ δy

60 IGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAV 119 ŏ

61 IGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKRAAFQWTWGKGVMLAGVV 120 g

120 TMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASALGFELSFKKSY 178 δ g

RESULT 2 A70207

Conserved hypothetical protein BBA01 - Lyme disease spirochete plasmid A/1p54 C; Species: Borralia burgdorferi (Lyme disease spirochete)
C; Species: Borralia burgdorferi (Lyme disease spirochete)
C; Species: Borralia burgdorferi (Lyme disease spirochete)
C; Species: Borralia burgdorferi (Lyme disease spirochete)
C; Species: Borralia burgdorferi (Lyme disease spirochete)
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Retrason, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, A; Authors: Smith, H.O.; Venter, J.C.
A; Fittle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID: 98065943; PMID: 9403685

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C;Species: Borrelia burgdorferi (Lywe disease spirochete)
C;Date: 13-Reb-1998 #sequence_revision 13-Reb-1998 #text_change 17-Mar-2000
C;Accession: F70243
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                                                                                                           A,Cross-references: GB.AE000790; NID:g2690224; PIDN:AAC66226.1; PID:g2690225; TICR:BBA01
A,Experimental source: strain B31
C;Genetics
A,Genome: plasmid
C;Superfamily: Lyme disease spirochete plasmid hypothetical protein BBA01
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-161 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 17-Mar-2000
C;Accession: G70239
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAG-AV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 GSFVQGDYIGGGGVLGFNLLGAILWGTGIILN~------HRETQLTGYILIGVGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 TMAVTRLT-EIIIPFTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASALGFELSFKKSY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 MAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASALGFELSFKKSY 178
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                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                          Query Match 32.5%; Score 293.5; DB 2
Best Local Similarity 41.1%; Pred. No. 9.6e-20;
Matches 74; Conservative 24; Mismatches 61
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G70239
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son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Natures 390, 580-586, 1997
A.Authors: Smith, H.O.; Venter, J.C.
A.Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A.Rocession: G70239
A.Accession: G70239
A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Molecule type: DNA
A.Residues: 1-190
A.K.Ebs
A.Cross-references: GB.AE000784; NID:g2690041; PIDN:AAC65989.1; PID:g2690045; TIGR:BB.A.Experimental source: strain B31
A.Genetics: A.Genome: plasmid
C.; Guperfamily: Lyme disease spirochete plasmid hypothetical protein BBA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTS system, maltose and glucose-specific IIABC component (malx) homolog - Lyme diseas C; Species: Borrella burgdorferi (Lyme disease spirochete)
C; Species: Borrella burgdorferi (Lyme disease spirochete)
C; Date: 13-Peb-1998 #sequence_revision 13-Feb-1998 #text_change 08-oct-1999
C; Accession: D70114
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whisterser, C.M.; Casjens, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hanson, M.; Vul. Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Reference numbor: A70100; MUID:98065943; PMID:9403685
A; Accession: D70114
A; Stelliminary; nucleic acid sequence not shown; translation not shown
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A.Residues: 1-574 <KLE>
A.Cross-references: GB:AE001124; GB:AE000783; NID:g2688003; PIDN:AAC66516.1; PID:g268|
A.Cross-references: GB:AEA01124; GB:AE000783; NID:g2688003; PIDN:AAC66516.1; PID:g268|
A.Experimental source: strain B31
C.Superfamily: phosphotransferase system glucose-specific enzyme II, factor II; phospi
F:15-527/Domain: phosphotransferase system glucose-specific enzyme II, factor II homol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 ALDKNAPKAAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTFANS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 IVVLLAFCVF-----SSFAQADDSKSAFNLGA-----GEKLLAYETSKKDPI--- 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 LLAYETSKK-DPIVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 26.5%; Score 240; DB 2; Similarity 39.6%; Pred. No. 9.1e-15; 57; Conservative 23; Mismatches 52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 YNRKLKNSLNIAFGGF----EPSFDINMGQASALGF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 EPSFDINMGQASALGFELSFKKSY 178
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Best Local Similarity
Matches 57; Conservat
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D70114
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probable c4-dicarboxylate transporter PA5169 [imported] - Agrobacterium tumefaciens probable c4-dicarboxylate transporter PA5169 [imported] - Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: 22-oct-2001 #sequence_revision 22-oct-2001 #text_change 11-Jan-2002 C; Accession: G98326 B; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Golda A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001 Plant Pathogen and Biotechnology Agent Agrobacterium A; Reference number: A97359; PMID:11743194 A; Sctatus: preliminary A; Molecule type: DNA A; Residues: 1-616 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ayacobacterium tumefaciens (Species: Agrobacterium tumefaciens (Strain C58, Duper C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 (Jaccession: AG2957) (Species: Ag3957) (Species: Ag3957) (Species: Ag3957) (Species: Ag3957) (Species: Agapt, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Worerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McC; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 (Species: Agapt, C317-2323, 2001 (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Agapt) (Species: Aga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 W-----TWGKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSF 158
   || :|| :| || ::|
301 LLTSVLFSGASGSSVANAAFGASTFQPELVKHGYPPAQAGAIIAA--TSVLDNVIPPSIA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 -FILINLFLGFGIGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKA--AFK 106
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                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 616;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 2.8; 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.7%; Score 87.5; 22.0%; Pred. No. 2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: linear chromosome
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Matches 42; Conservative
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RQSAGEAAAIG 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: AGR_L_3113
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G98325
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F75346
phosphor-acetylmuramoyl-pentapeptide- transferase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: F75346
R;White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
K, M.; Shen, M.; Vannathevan, J.C.; Eraser, C.M.
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
A;Itle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75346
A;Accession: F75346
A;Accession: F75346
A;Accession: F75346
A;Cross-references: GB:AE002024; GB:AE000513; NID:g6459614; PIDN:AAF11390.1; PID:g645961
C;Genetics:
A;Gene: DR1835
A;Map position: 1
C;Superfamily: phospho-N-acetylmuramoyl-pentapeptide-transferase
                                                                                                                                              R.J.;
C.; Ma
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A; Molecule type: DNA
A; Molecule type: DNA
A; Rosidues: 1-469 < KURN
A; Cross-references: GB: AEO01437; PIDN: AAK79307.1; PID: q15024271; GSPDB: GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics:
A; Genetics: CAC1339
C; Superfamily: glucose transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 VISSIMVGGVLGVGFSGFL---GDAIGRRKVLMLAAALFAISAVISSISTSAFMLIFARI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 GIGSFAQGDILG----GFLILGFDAVGIG--LILTGAYLDIKALDKNAPKAAFKWTWGK- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LIVVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKKDPIVPFLLNLF-----LGF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LLFIVLISCA------AGLGGLLYGYDTAVISCAIGFLKKLYNLSPAMQGF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 AYETSKKDPIVPFLLNLFLGFGIGSFAQGDILGGFLILG----FDAVGIGLILTGAYLDI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 --GMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNI-AFGGFEPSFDINMG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
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;
350 FTAPLLYFVHAAYSGFALLLANFFNVTIGNSFSTGF 385
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9.9%; Score 89.5; Di
Best Local Similarity 25.1%; Pred. No. 1.4;
Matches 44; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Matches 40; Conserv
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A; Residues: 1-363 <GLA>
                         A;Status: preliminary
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R; Hatzoglou, E.; Rodakis, G.C.; Lecanidou, R.
Renetics 140, 1353-1366, 1995
A; Title: Complete sequence and gene organization of the mitochondrial genome of the land A; Reference number: S59143; MUID:96120351; PMID:7498775
A; Accession: S59143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein jhp0131 - Helicobacter pylori (strain J99)
C; Species: Helicobacter pylori
A; Variety: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Aug-1999
C; Accession: F71969
R; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Tavs, C.; Gibson, R; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Artile: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: X83390; NID: 9975668; PIDN: CAA58296.1; PID: 9975669; GSPDB: GN001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - land snail mitochondrion C;Species: mitochondrion Albinaria coerulea (land snail)
C;Date: 19-Mar_1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
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301 LLTSVLFSGASGSSVANAAFGASTFQPELVKHGYPPAQAGAIIAA--TSVLDNVIPPSIA 358
                                                                                                                                                                                            50 -FLLNLFLGFGIGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKA--AFK 106
                                                                                                                                                                                                                                                    107 W-----TWGKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSF 158
                                                                                                                                                                                                                                                                              63 FAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAVTMA 122
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                                                                                    -----AGEKLLAYETSKKDPIVP---- 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.6%; Score 86.5; DB 2; Length 545; Best Local Similarity 29.1%; Pred. No. 3.1; Matches 39; Conservative 21; Mismatches 37; Indels 3
Length 616;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
    DB 2;
9.7%; Score 87.5; DE
22.0%; Pred. No. 2.8;
                                           Conservative 35; Mismatches
                                                                                  9 LLAFCVFSSFAQADDSKSAFNLG------
                       22.0%;
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                                                                                                                                                                                                                                                                                                                                    DINMGQASALG 169
                                                                                                                                                                                                                                                                                                                                                                           468 ROSAGEAAAIG 478
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A; Residues: 1-545 <HAT>
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Genome: mitochondrion
A,Genetic code: SGC4
A,Start codon: ATT
                                         42;
                         Best Local
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                                                                                                                                                                                                                                                                                                                                    159
                                         Matches
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GB:AE001439; NID:g4154639; PIDN:AAD05710.1; PID:g415
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PTS system, fructose-specific enzyme IIC component homolog lin2240 [imported] - Listc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ridlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A., Ok, C.; Schlueter, T.; Simces, N.; Teierez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Accession: AE7712
A;Status: Preliminary
A;Molecule type: DNA
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AG1341
PTS system, fructose-specific enzyme IIC component homolog lmo2135 [imported] - Liste C; Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG1341
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A; Experimental source: strain Clip11262
C; Genetics:
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AE1712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 ----PK------WAQGLMPMMIIPLISSLVIGLLMYFVVGVPIVWATEAMTSFLQGMQGS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                            :::||:||| |: :||:||| 305 IVWVLMAFCKIVSYEDIIKNKSAFNIFLLGSLLTMAGGLKNVGFLNFIGNAAQNFLEHA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 HLDPLIAVLFIVALFYLSHYFFASITAHVSALFALFVGIGSHIQGVNLQELSLFLMLSLG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 IAYSIADRPGIAPGLLMGLIANSIGAGFLGGMLGGYL-----VGYFVLILVKYLKV--- 121
                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
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                                                                                                                                                                                                                                                                                                                                  39; Indels
                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 AVGI-----GLILTGA-YLDIKALDKNAPKAAFKWTWG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 IMGILTPYGTGPSTIYYGSGYIQSKDF------WKWG 455
                                                                                                                                                                                                                                                                       DB 2;
A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-482 <ARNA A; Cross-references: GB: Ab001452; GB: Ab001439; NID A; Experimental source: strain J99 C; Genetics: A; Gene: jhpol31 C; Superfamily: 2-oxoglutarate/malate translocator
                                                                                                                                                                                                                                                                9.5%; Score 85.5; Dilarity 24.2%; Pred. No. 3.3; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.4%; Score 85; DB 23.5%; Pred. No. 2.8;
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1341
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C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 22-Oct-1999
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C:Accession: A41901; S27687
J. Bacteriol. 174, 3651-3658, 1992
A:Title: Sequence and transcriptional analysis of the Streptomyces glaucescens tcmAR tet
A:Reference number: A41901; MUID:92276347; PMID:1592819
A:Contents: GIAA.O, ETH 22794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A41901
metabolite export pump of tetracenomycin C resistance TcmA - Streptomyces glaucescens
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A:Molecule type: DNA
A:Residues: 1-538 cGUI>
A:Cross-references: EMBL:M80674; NID:q153488; PIDN:AAA67509.1; PID:g153490
A:Cross-references: EMBL:M80674; NID:g153488; PIDN:AAA67509.1; PID:g153490
A:Note: sequence extracted from NCBI backbone (NCBIP:104630)
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C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 DKNAPKAAFKWTWGKGMM-----LAGAVTMAVTRLTEIIIPFTFA----NSYNRKLKNS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 IAYSIADRPGIAPGLLMGLIANSIGAGFLGGMLGGYL-----VGYFVLILVKYLKV--- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------TMAVT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32;
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Best Local Similarity 24.6%; Pred. No. 4.2;
Matches 33; Conservative 19; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.4%; Score 85; DB 2; Best Local Similarity 23.5%; Pred. No. 2.8; Matches 32; Conservative 26; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 LNIAFG---GFEPSFD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 MRFVFGAVLGAMAAFD 187
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RESULT 15 T19495

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A;Introns: 61/1; 98/3; 191/1; 220/3; 268/3; 340/1; 392/2; 475/2; 496/3; 537/1; 588/1
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hypothetical protein C27A7.3 - Caenorhabditis elegans
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C; Accession: T19495
B; Harris, B.
Submitted to the EMBL Data Library, October 1996
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9.3%; Score 84.5; DB 2;
Best Local Similarity 24.0%; Pred. No. 5.8;
Matches 37; Conservative 21; Mismatches 47;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2003, 14:25:51; Search time 10.0562 Seconds Run on:

(without alignments) 820.439 Million cell updates/sec

US-09-508-487-19 902

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

199416 seqs, 46092074 residues Searched:

[otal number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications AA: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 48, Appl	Sequence 3606, Ap	Sequence 13341, A	Sequence 4875, Ap	Sequence 13924, A	Sequence 6850, Ap	Sequence 5811, Ap	Sequence 6860, Ap	Sequence 20, Appl	Sequence 20, Appl	Sequence 11951, A	Sequence 5024, Ap	Sequence 10165, A	Sequence 422, App	Sequence 4062, Ap	Sequence 5144, Ap	Sequence 14, Appl	Sequence 20, Appl	Segmence 2 Appli
	ID	US-10-260-877-48	US-09-738-626-3606	US-09-815-242-13341	US-09-738-626-4875	US-09-815-242-13924	US-09-738-626-6850	US-09-738-626-5811	US-09-738-626-6860	US-10-051-902-20	US-10-051-909-20	US-09-815-242-11951	US-09-738-626-5024	US-09-815-242-10165	US-09-741-669-422	US-09-738-626-4062	US-09-815-242-5144	US-09-965-536A-14	US-08-910-386A-20	0-664-836-80-20
	DB	. 6	6	10	6	10	6	0	6	6	6	10	6	10	10	φ	10	φ	8	σ
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æ	Query Match	9.4	9.3	8.9	8.9	8.8	8.8	8.8	8.7	9.0	8.6	8.3	8.3	8.2	8.1	8.0	8.0	8.0	8.0	0
	Score	84.5	83.5	80.5	80	79.5	79.5	79	78.5	77.5	77.5	74.5	74.5	74	73	72.5	72.5	72.5	72.5	72.5
\	Result No.	-	7	e	4	2	9	7	8	6	10	11	12	13	14	15	. 16	17	18	19

; Sequence 3606, Application US/09738626; Publication No. US20020197605A1

RESULT 2 US-09-738-626-3606

Sequence 5, Appli Sequence 3800, Ap Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 25, Appl Sequence 109, Appl Sequence 109, Appl Sequence 1003, A Sequence 1003, A Sequence 100 Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13218, A Sequence 13218, A Sequence 2, Appli Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 33, Appl Sequence 34, Appl Sequence 3676, Appl Sequence 3676, Appl Sequence 3676, Appl Sequence 3676, Appl Sequence 3676, Appl Sequence 13058, Appl
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ALIGNMENTS

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Sequence 48, Application US/10260877

Sequence 48, Application US/2030021813A1

GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Hessler, Paul E.
APPLICANT: Hessler, Paul E.
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APPLICANT: Howerlow: SCANNING IN HAEMOPHILUS INFLUENZAE FOR THE IDENTIFICATION OF
TITLE OF INVENTION: SSSENTIAL GENES'
TITLE OF INVENTION: SSSENTIAL GENES'
TITLE OF INVENTION UNMBER: US/10/260,877
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US/99/649,145
PRIOR APPLICATION NUMBER: US/99/649,145
SPRIOR PLING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 137
SEQ ID NO 48
LENGTH: 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRGANISM: H. influenzae
US-10-260-877-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 34; Conserv
US-10-260-877-48
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60 -----GIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALD--GITKKAAFQWTWGK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 SSFAQANDSKNGAF--GMSAGEKLLV-----YETSKQDPIVPFLLNLFLGF---- 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 VNIPMAAINTAMNDFLGG--LGGGSAVLLGIVLGG----MAAVDMGGPVNKAAY--VFGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 GVMLA-----GVVTMA------VTRLTEIILPFTFANSYNRKLKNS--LNVALG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.9%; Score 80; DB 9; Length 487; Best Local Similarity 22.3%; Pred. No. 1.7; Matches 37; Conservative 19; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.9%; Score 80.5; DB 10; Best Local Similarity 25.7%; Pred. No. 2.2; Matches 45; Conservative 25; Mismatches 60;
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 13341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4875, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4875
                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Streptococcus pneumoniae US-09-815-242-13341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-738-626-4875
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                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 -----GLVVSAGTAWAGRLRGASGVTLAGIILTAGFWMGPIVTSGLGMASTSIITPFA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 VFIGVTILLFTAGWAANHFASVLVLIREQLDVSSVLVNGAFGIYALGLLPSLLAGGVLAD 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 --GEKLLVYETSKQDPIVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILAGAY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 FANSYNRKLKNSLNVALGGF -----EPSFDVAMGQSSALGFELSFKKS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 IS-----VALSLIAVVVGFALGDARSTPS---ALGASSGIKHERSMKKA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 IFVLATFCVFSSFAQANDSK-------NGAFGMSA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Wanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in FILE OF INVENTION:
FILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.3%; Score 83.5; DB Best Local Similarity 24.3%; Pred. No. 0.56; Matches 56; Conservative 24; Mismatches
                                                                                                                              APPLICANT: OCHIAI, KEINO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
TILLE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRICH APPLICATION NUMBER: 60/191,078
PRICH FILING DATE: 2000-03-21
PRICH APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13341, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                        MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                              NAKAGAWA, SATOSHI
                                                                                                          HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-815-242-13341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3606
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US-09-738-626-5811
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APPLICANT:
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                                                                                                                                                                                                         APPLICANT:
APPLICANT:
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253 IMIVAAFALFAWF-----IYQQSRAEK----SGNDPLVPLEIFKFRNFSLGNIC 297
                                                                                 66 QGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVWLAGVVTMAVT 125
                                                                                                                                                          -----IMAMGFTVAGTPLPIMLY-----FQQAHGMNAMEAGFMMVPQA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: | |:: | :: | |:: | |: |: | | |: |: | |:: | |:: | |:: | |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 VYETSKQDPI-----VPFLLNLFLG--FGIGSFAQGDILGGSLILGFDAVGIGLILAGA 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: 279X10, JUGICA W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tarmouto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT PEPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-22
PRIOR PILING DATE: 2001-02-22
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                                                                                                                                                                                                                                           126 RLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAMGQSSALGF 171
                                                                                                                                                                                                                                                                                              39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13924, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-738-626-6850
Sequence 6850, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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Zyskind, Judith W.
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S-09-815-242-13924
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Best Local Similarity
Matches 39; Conserv
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100 ITKKAAFQWTWGKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEP-- 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 PIVP-FLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILAGA----YLDIKAL--DG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 417;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50;
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24.7%; Pred. No. 1.6;
tive 22; Mismatches 50;
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                                                                                                                                                  AFFLICANT: OZAKT, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SPRIOR FILING DATE: 2000-04-07
SPRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SEQ ID NO 5811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5811, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSHI
                  HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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ANDO, SEIKO
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Best Local Similarity
Matches 39; Conserv
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Sequence 20, Application US/10051902
Patent No. US20020178468A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Allen, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 26.09
Matches 32; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                               ; LENGTH: 513
; TYPE: PRT
; ORGANISM: Zea mays
US-10-051-902-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 AVT 125
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  US-10-051-902-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Zee
US-10-051-909-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 LTIILATAGFDAWIVVGVGALLLGILMVS------LP-AFAHPWTRRITGDDSIAIGH 187
                                                                                                                                    30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 GMSAGEKLLV----YETSKQDPIV-PFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIG 84
                                                                                                                                                                                                                                                                          85 LI------UAGAYLDIKALDGITKKAAFQWTWGKG-----VMLAGVVTMA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 VP-FLLNLFLGFGIGSFAQ--GDILGGSL--ILGFDAVGIGLILAGAYLD----
                                                                                    DB 9; Length 346;
                                                                                                                                  33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                          Query Match
8.8%; Score 79; DB 9
Best Local Similarity 27.0%; Pred. No. 1.5;
Matches 30; Conservative 18; Mismatches
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8.7%; Score 78.5; DE
Best Local Similarity 20.0%; Pred. No. 2.6;
Matches 38; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFRENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SOFTWARE: PatentIn ver. 3.0
                ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5811
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6860, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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US-09-738-626-6860
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAYASHI, MIKIRO
COCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKTHIRO
IKEDA, MASATO
OZAKI, AKIO
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LENGTH: 513
LENGTH: 346
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APPLICANT:
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63 SFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGKGVMLAGVVTM 122
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APPLICANT: Hitz, Bill
APPLICANT: Hitz, Bill
APPLICANT: Kinney, Tony
APPLICANT: Tringey, Scott
TITLE OF INVENTION Plant Sugar Transport Proteins
FILE REFERENCE: B8-1163
CURRENT APPLICATION NUMBER: US/10/051,902
CURRENT FILING DATE: 202-01-17
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/291,922
PRIOR FILING DATE: BARLIER FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EILIGILSLYSLFGSFAGARTSDR-----IGRRLTVV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 513;
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Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30; Indels
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APPLICANT: Helentjaris, Tim
APPLICANT: Hitz, Bill
APPLICANT: Hitz, Bill
APPLICANT: Kinney, Tony
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: Ball63 US CIP
CURRENT APPLICATION NUMBER: US/10/051,909
CURRENT FILING DATE: 2002-01-17
PRIOR FILING DATE: April 24, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.6%; Score 77.5; DB 9; 26.0%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Mismatches
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Publication No. US20020199217A1
GENERAL INFORMATION:
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93 -FAAVIFFVGSLLMGF-AVNYGMLMAGRFV---AGVGV-------GYGGMIAPVYTA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 GAFAFGVLNRLLIVTG-----LHHILNNLVWFVFGSFTDPETGRVVTGDLARYFAGDPK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 GGSLILG-FDAVGIGL-------ILAGAYLDIKA---LDGITKKAAFQWT 109
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: WINYENTON: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
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Best Local Similarity 22.9%; Pred. No. 7.7;
Matches 39; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11951
LEMCTH: 570
                                                                                                                                                                                                                                Sequence 11951, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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Sequence 5024, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas aeruginosa US-09-815-242-11951
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
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TITLE GOT INVERTIONS (1909-138) 6.36
FILLS BEREBRENE: 19-13-13
CURRENT PERLICATION MENDRE: 19-09-13-18
THE GOT INVERTIONS (1900-14-18)
PRICOS PLICATION MENDRE: 19-09-13-18
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PRICOS APPLICANT: MENDRE: 19-09-13-18
PRICOS PRICOS APPLICATION MENBRE: 10-03-13-18
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                                                                                                                                                                                                                                                                      113 ------GVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFDVAM 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 PIVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 PIVIIIFSKILG-----MKAGDCFKAGLHIGIGFVGIGLVI-GLMLD---SIGPAAKAMA 69
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                                                                                                                                                                    Length 417;
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                                                                                                                                                                                                                                               64 FAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKKAAFQWTWGK---
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Patent No. US20020022718A1
GENERAL INFORMATION:
APPLICANT: FORSYth:
APPLICANT: JOHSEN, Kari L.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli
FILE REFERENCE: ELITRA, 009A
CURRENT APLICATION NUMBER: US/09/741,669
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FASTERQ for Windows Version 4.0
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                                                                                                                                                                DB 10;
                                                                                                                                                              Query Match
8.2%; Score 74; DB 1
Best Local Similarity 24.6%; Pred. No. 6;
Matches 31; Conservative 23; Mismatches
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26.4%; Pred. No. 8.3;
tive 12; Mismatches
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10165
LENGTH: 417
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Publication No. US20020197605A1
GENERAL INFORMATION:
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHKO
APPLICANT: YOKOI, HARUHKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 26.4%
Matches 29; Conservative
                                                                             ; TYPE:.PRT; ORGANISM: Escherichia coli
US-09-815-242-10165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Escherichia coli
09-741-669-422
                                                                                                                                                                                                                                                                                                                                                                                                           164 GQSSAL 169
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US-09-741-669-422
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Search completed: March 14, 2003, 14:37:03 Job time: 12.0562 secs

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GenCore version 5.1.4_p5_4578

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OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 20:13:37; Search time 33.8253 Seconds

(without alignments)
7815.311 Million cell updates/sec
Perfect score: 862
Sequence: 1 gattttcattggatcccag......atattttatttctctgctaa 862
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 441362 seqs, 153338381 residues
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Total number of hits satisfying chosen parameters: 882

Inimum DB seq length: 0 . Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Issued_Patents_NA:*
1: \cgn2_6\ptodata1/\ina/5A_COMB.seq:*
2: \cgn2_6\ptodata1/\ina/5B_COMB.seq:*
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4: \cgn2_6\ptodata1/\ina/6B_COMB.seq:*
5: \cgn2_6\ptodata1/\ina/FB_COMB.seq:*
6: \cgn2_6\ptodata1/\ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appli	Appli Appli	Appli	Appl	Appli	Appli	Appli	App	Appl	App	App	App	Appl	Appli	Appli	Appli	Appli	Appli	Appl	App	Appl	Appl	Appl	Appl	Appl	App
Description	ਜੇ	Sequence 3, 7	, ,	11,	3,	Sequence 1, 1	Sequence 1, 1	Seguence 224,	Sequence 36,	Sequence 651,		Sequence 534,	Sequence 32,	Sequence 4, 1	Sequence 8, 1	Ļ	٦,	Sequence 1, 1	13,	Seguence 972,	Sequence 27,	Sequence 20,	Sequence 21,	Sequence 22,	Sequence 10,	Sequence 595,
ID	US-09-056-075-1	US-U8-319-704-5 US-09-410-028-3	US-09-056-075-1	US-08-991-677-11	US-08-913-842-3	US-09-014-583-1	US-08-485-284A-1	US-08-998-416-224	US-07-872-678A-36	US-09-641-638-651	US-08-998-416-288	US-08-998-416-534	US-08-617-860B-32	US-08-605-106-4	US-08-936-107A-8	US-08-463-048-1	US-08-463-229-1	US-08-302-891-1	US-08-487-826B-13	US-08-998-416-972	US-08-817-926-27	US-08-724-394A-20	US-08-724-394A-21	US-08-724-394A-22	us-09-791-211-10	US-08-998-416-595
DB	77	٦ ٣	7	4	٣	m	7	4	7	4	4	4	٣	~	4	Н	Н	~	7	4	٣	~	7	7	4	4
% Query Match Length DB	6243	3077	6243	2251	2960	734	1667	782	3618	20674	837	854	1850	4098	5064	1972	1972	1972	19124	688	4818	246240	246240	246240	98844	658
& Query Match	5.7	5.7	5.5	5.5	5.4	5.3	5.3	5.2	5.2	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.0	5.0	5.0	5.0	4.9
Score	49.2	4 4 2 0	47.6	47.2	46.2	45.8	45.8	45.2	45.2	44.2	44	44	44	44	44	43.8	43.8	43.8	43.8	43.6	43.6	43.4	43.4	43.4	42.8	42.4
Result No.	c 7	7 M	4	'n	9 0	7	ω ·	ο 0	c 10	11	12	13	c 14	c 15	16	c 17	c 18	c 19	c 20	21	22	23	24	25	c 26	27

Sequence 971, Applin Sequence 2, Applin Sequence 3, Applin Sequence 4, Applin Sequence 4, Applin Sequence 1137, Appling Sequence 11, Applin Sequen	Sequence 1, Appli Sequence 7, Appli Sequence 191, App Sequence 287, App
US-08-998-416-971 US-07-867-106-4 US-07-867-106-2 US-09-103-478-3 US-09-103-478-4 US-09-103-478-4 US-09-193-931C-4 US-08-918-416-1137 US-08-617-8608-32 US-08-65-106-4 US-09-868-111 US-07-872-678A-36 US-07-872-678A-36	US-09-150-741-1 US-09-462-136-7 US-08-998-416-191 US-08-998-416-287
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740 31385 3395 3395 3395 3395 7560 7560 1850 4098 1826 1826 1826 3618	8920 11459 663 860
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228 233 332 334 337 440 440	4 4 4 4 5
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ALIGNMENTS

Query Match 5.7%; Score 49.2; DB 2; Length 6243; Best Local Similarity 58.0%; Pred. No. 0.046;

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us-09-508-487-20.rni

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ASPARAGINE RESIDUE-SPECIFIC ENDOPROTEASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1748 TGAACCTTAAAGTTATACTAACATTGCTAAATGATACAAGCTAGTGGAAAGTTGGGAATT 1807
    271 AATTAAAAATTTATTTATTAATTCAATTATAATCCAATATAAGCATATAAATTTAAGATT 330
                                                                                                                    331 TICTICAAAGTATATATCTITATTITAATCTTAAACTTTTCTTGAAAATGAAAATCAATA 390
                                          236 IGTTGTTTTGCTAGCCTTTTGTGTTTTTTTTTAGCTTTGCTCAAGGCTGATGATTCTAAAAG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 AGCTCTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAAGTTAAAATTTAAATAGTTT 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 TITIATGAATAAATTTTAAATGTTGTTTTGCTAGCCTTTTGTGTTTTTTTGTAGCTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 TAAAAAACCTTTTTTAAATTTCATTAATATGTTACTATAATACCAGTTTTAATAAAGAGGT
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Pred. No. 0.044;
0; Mismatches 145; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ARAHIRA, Masaomi
APPLICANT: FUKAZAWA, Chikafusa
TITLE OF INVENTION: PLANT-DERIVED, ASPARAGINE
TITLE OF INVENTION: CDNA AND A GENE
FILE REFERENCE: 8361-0007-0
CURRENT APPLICATION NUMBER: US/09/410,028
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: JP 327537/1998
EARLIER FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 3
                                                                                                                                                                                                                       356 TATTGTGCCATTTTTATTGAACCTTTTTT 384
                                                                                                                                                                                                                                                                                                                5-09-410-028-3
Sequence 3, Application US/09410028
Patent No. 6107471
GENERAL INFORMATION:
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Matches 136; Conservative
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; LOCATION: (2707)..(2895)
US-09-410-028-3
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LOCATION: (1160)..(1300)
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                                                                            Gaps
                                      123 ATACTITGAAAAAGTITAAATTTAAATAGTTTTAAAAACCTTTTTAAAATTTCATTAATA 182
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hoffman, Stephen L.
APPLICANT: Charcenvit, Yupin
APPLICANT: Charcenvit, Yupin
APPLICANT: Hedstrom, Richard C.
APPLICANT: Doolan, Denise L.
TITLE OF INVENTION: Protective 17 kDa Malaria Hepatic and
TITLE OF INVENTION: Erythrocytic Stage Immunogen and Gene
CORRESPONDENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1422; 0.038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.7%; Score 49; DB 1; Length 142
Best Local Similarity 46.8%; Pred. No. 0.038;
Matches 154; Conservative 0; Mismatches 175; Indels
    Indels
  63;
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PAPLICATION NUMBER: US/08/319,704
FILING DATE: 07-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Naval Medical R & D Command
Bldg 1, T-12, 8901 Wisconsin Avenue
  Mismatches
                                                                                                                                                                                                                       243 TTGCTAGCCTTTTGTGTTTTTTTTTTTTT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08319704 Patent No. 5814617 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFO TATA
NAME: A David Spewack
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: 75,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (301) 295-6759
TELEFAX: (301) 295-1022
INFORMATION FOR SEO ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1422 base pairs
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Bethesda
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
87;
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                                                                                                                                                                                                                                                                                                              US-08-319-704-5
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Matches
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3030 TATAAATTATGATTATTCCAAAGATACTAAAGATTTAATTTTTCAATTTTAACAATAC 3089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 AATITCAITAATAIGTIACTATAATACCAGITITAATAAAGAGGITTTTAIGAATAAATT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 TITAAITGITGITTTGCTAGCCTTTTGIGITTTTTTTTGTGCTTTGCCTCAAGCTGAIGAITC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 11, Application US/08991677A
; Sequence 11, Application US/08991677A
; Patent No. 6252135
; GENERAL INFORMATION:
    APPLICANT: Chiang, Vincent L
    APPLICANT: Carraway, Daniel T
    APPLICANT: Smeltzer, Richard H
    TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
    FILE REFERENCE: 5061
    CURRENT APPLICATION NUMBER: US/08/991,677A
    CURRENT FILING DATE: 1997-12-16
    EARLIER FILING DATE: 1997-12-16
    NUMBER OF SEQ ID NOS: 11
    NUMBER OF SEQ ID NOS: 11
    SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 AAAAACTTTTAGCTTATGAAACTAGTAAGAAAGATCCTATTGTGCCATTTTTATTGAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08913842
Patent No. 6028250
GENERAL INFORMATION:
APPLICANT: OHBA, TOSHIharu
APPLICANT: ANMA, YOSHIKO
APPLICANT: ANMA, YOSHIKO
APPLICANT: KATO, IKUNOSHIN
TITLE OF INVENTION: PLANT PROMOTER AND METHOD FOR GENE
TITLE OF INVENTION: EXPRESSION USING SAID PROMOTER
NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47.2; DI
Pred. No. 0.1;
                                                                                                                                                                                3090 TITITGTAATATTATGTTTAAATTTG 3119
                                                                                                                                           379 ITTITIAGGGTTTGGAATAGGTTCTTTG 408
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Matches 121; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Pinus taeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAA 862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAATTTAAATAGTTTTAAAAACCTTTTTTAAATTTCATTAATATGTTACTATAATACCA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 TITITICTAGCTITGCTCAAGCTGATGATTCTAAAAGCGCTTTTAATTTGGGAGCGGGAG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 3770..4013
OTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit) from
OTHER INFORMATION: plasmid RP4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAATTIGTAGAATTITGGACAAATAAAGACATTATTAAAAGAATTGAAATTGCTAATTT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6243;
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                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Johnson, Eric A.
APPLICANT: Bradshaw, Marite
APPLICANT: Rood, Julian
TITLE OF INVENTION: Expression System for Clostridium
TITLE OF INVENTION: Species
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47.6; DB 2;
Pred. No. 0.1;
0; Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  960296.95238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   ; Sequence 1, Application US/09056075
; Patent No. 5955368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-500
TELEFRAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: Quarles & Brady
STREET: 1 South Pinckney S
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 6243 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 53701-2113
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                         as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                             RESULT 4
US-09-056-075-1
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Best Local (
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485 TTTAAATTCTATTTTATTTTAATTCTTTCTTTATCATAGTTATCATATAACAA--TTATA 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 ATAAAAAATTTATATTTAAATGAATTAATTTCCTTTTATTTTTAATAATACGTTAATTCT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 AAACCTTTTTAAATTTCATTAATATGTTACTATAATACCAGTTTTAATAAAGAGGTTTT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 ACAAATAAAGACATTATTAAAAGAATTGAAATTGCTAATTTTATGGTCAAATCAAGAGC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08485284A
Patent No. 5750372
GENERAL INFORMATION:
APPLICANT: SAKAI, YASUYOSHI
APPLICANT: TANI, YOSHIKI
APPLICANT: SHIBANO, YUJI
APPLICANT: KONDO, HIROTO
APPLICANT: HATANAKA, HARUYO
TITLE OF INVENTION: NOVEL VECTOR HAVING PROMOTER THAT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 AGCTGATGATTCTAAAAGCGCTTTTAATTTGGGAGCGGGAGAAAAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BURNS, DOANE, SWECKER & MATHIS, L.L.P.
                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,583 FILING DATE: 28-JAN-1998 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: JP 200398/96 FILING DATE: 30-JUL-1996 ATTORNEY/AGGETY INCRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.3%; Score 45.8; DB 3; Best Local Similarity 49.8%; Pred. No. 0.16; Matches 143; Conservative 0; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Teskin, Robin L.
REGISTATION NUMBER: 35,030
REFERRNCE/DOCKET NUMBER: 027066-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Candida boldinii
) DEVELOPMENTAL STAGE: wild type
US-09-014-583-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
                                                                           : Virginia
RY: United States
22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 734 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
  ADDRESSEE: BURNS, DOAN
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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MOLECULE TYPE: D
ORIGINAL SOURCE:
                                                                           STATE: Vi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 CAAGAAGCTCTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAGTTAAAATTTAAAT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 AGTITIAAAAACCIITITIAAATITICAITAATAIGITACTATAATACCAGTITIAAATAA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 AATTTTCGACAAATAAAGACATTATTAAAAGAATTGAAATTGCTAATTTTATGGTCAAAT 89
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Pred. No. 0.17;
0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 GAGGTTTTTATGAATAAATTTTTAATTGTTGTTTTTGCTAGCCTTTTG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHOD FOR PRODUCING PHYTASE NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
SEE: BROWDY AND NEIMARK, P.L.L.C.: 419 7th Street N.W., Ste. 300 Washington
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 07-073043
FILING DATE: 30-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00777
FILING DATE: 26-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,842
                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09014583
Patent No. 6140077
GENERAL INFORMATION:
APPLICANT: NAKAMURA, Takeshi
APPLICANT: SUZUKI, Tadashi
APPLICANT: KATO, No. 614007 uo
APPLICANT: SARI, Yasuyoshi
APPLICANT: MOCHIZUKI, Daisuke
APPLICANT: MOCHIZUKI, Daisuke
APPLICANT: TAKRHASHI, Hitoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/POCKET NUMBER: 04Ba-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
ITELEPHONE: (202) 737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERETSTICS:
LENGTH: 2960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.4%;
Best Local Similarity 50.2%;
Matches 114; Conservative
                                                                                                                                                                         Floppy disk
                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                      20004
  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-913-842-3
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ADDRESSEE:
                                       APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1426 ТТТАААТТСТАТТТТАТТТТААТТСТТТСТТТАТСАТАСТТАТСАТАТААСАА--ТТАТА 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 TCTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAGTTAAATTTAAATAGTTTAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 ACAAATAAAGACATTATTAAAAGAATTGAAATTGCTAATTTTTATGGTCAAATCAAGAAGC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 AAACCTTTTTAAATTTCATTAATATGTTACTATAATACCAGTTTTAATAAAGAGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1667;
FITLE OF INVENTION: INDUCIBLE BY METHANOL AND/OR GLYCEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45.8; DB 1; Length 1
Pred. No. 0.19;
0; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 AGCTGATGATTCTAAAAGCGCTTTTAATTTGGGAGCGGGAGAAAAC 324
                                                                                                                  STATE: D. C.
COUNTRY: U.S.A.
ZIP: 2005-3918
COMPUTEN READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTEN: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,284A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217755/FPS38209US
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 43361/1992
FILING DATE: 28-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/025,416
FILING DATE: 01-MAR-1993
ATTONEY AGENT INFORMATION:
NAME: WHITE JR., PAUL E.
REGISTATION NUMBER: 32,017
                NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN DARBY & CUSHMAN,
STREET: 1100 New YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 224, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 2177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.3%;
Best Local Similarity 49.8%;
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: genomic DNA
US-08-485-284A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1667 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                 Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-08-998-416-224/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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464 AAATAGAAATATTACTAGACTAATAAAATAAATATTATGAAAGGAACATTTAATAATTA 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 ACCTTTTTAAATTTCATTAATATGTTACTATAATACCAGTTTTAATAAAGAGGTTTTTA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 ITAATAAACITAATAATCTATTTATTAAAAAATGGTATATTTAATAAAATTAAAT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 TGAATAAATTTTTAATTGTTGTTTTGCTAGCCTTTTGTGTTTTTTCTAGCTTTGCTCAAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 AAATAAAGACATTATTAAAAGAATTGAAATTGCTAATTTTATGGTCAAATCAAGAAGCTC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 782;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC.1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC.1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.2%; Score 45.2; DB 4; Best Local Similarity 48.1%; Pred. No. 0.22; Matches 128; Conservative 0; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF/5-30306/A/CGC1976
                                                                                                                                                                                                       No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 CTGATGATTCTAAAAGCGCTTTTAAT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 ATGTTTTATGTTAAATAGATAATAAT 199
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-07-872-678A-36/c
: Sequence 36, Application US/07872678A
                                                                                                                                                                                                                       STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF,
TELECOMMUNICATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 782 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 919-5-1
TELEPHONE: 919-541-8689
                                                APPLICANT: Knechtle, Ph.
APPLICANT: Rebischung, CTITLE OF INVENTION: GENUTILE OF INVENTION: AND NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: PAG1208UP
US-08-998-416-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
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OTHER INFORMATION: 10-508-245 : polymorphic base C or T NAME/KEY: allele LOCATION: 1559
OTHER INFORMATION: 10-509-284 : polymorphic base C or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : polymorphic base C or T
  CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 1090-02-11
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-13
PRIOR FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 1304
SEQ ID NO 651
LENGTH: 20674
                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 5'regulatory region NAME/KEY: exon LOCATION: 3124..3297
OTHER INFORMATION: exon 1
MAME/KEY: exon 1
LOCATION: 1124..3297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191
NAME/KEY: allele
LOCATION: 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc_feature
COCATION: 17555..20674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: exon 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: exon 11
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OTHER INFORMATION: exon 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 8645..8854
OTHER INFORMATION: exon 8
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 12254..12340
OTHER INFORMATION: exon 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: exon 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: exon 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: exon 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: 5552..5633
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 3871..4072
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12854..13023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 13308..13429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16567..16667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 5758..5880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 6349..6509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 651, Application US/09641638
Patent No. 6432648
Patent No. 6432648
Patent No. 6432648
PAPLICANT: Blumenfeld, Marta
APPLICANT: Bouqueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REPERENCE: GENEST: 051CP1
CURRENT APPLICATION NUMBER: US/09/641,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2910 TITITAATAATITTAATATITTAATAAATAATATGITAAATITAAATTAAATGITAAATT 2851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 AGACATTATTAAAAGAATTGAAATTGCTAATTTTATGGTCAAATCAAGAAGCTCTATTGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 GAAGCGAATTTCAAGTAATACTTTGAAAAAGTTAAATTTAAATAGTTTTAAAAACCTTT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 TITAAATITCATTAATATGITACTATAATACCAGTITITAATAAAGAGGITTTTATGAATA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                           APPLICANT: Bell, Graeme, et al.
TITLE OF INVENTION: DETECTION OF EARLY-ONSET
TITLE OF INVENTION: NON-INSULIN-DEPENDENT DIABETES MELLITUS
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: Post Office Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.2%; Score 45.2; DB 1; Length 3618; 52.1%; Pred. No. 0.29; tive 0; Mismatches 93; Indels 0
                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: FIDEPY WISK
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS'
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/872,678A
FILING DATE: 22-APRIL-1992
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: COUGHLIN, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/POCKET NUMBER: 36,111
REFERENCE/POCKET NUMBER: ARCDOIG
TELEPAN: 713-787-1400
TELEPAN: 713-789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-872-678A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.2%
Best Local Similarity 52.1%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 77210
COMPUTER READABLE FORM:
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                        GENERAL INFORMATION:
                                                                                                                                                                                                            Houston
Patent No. 5541060
                                                                                                                                                                                                                                         Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-641-638-651
                                                                                                                                                                                                                                 STATE: To COUNTRY:
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f C	motif ATTTA or	base C or T	of T	base G or C	c base A or G	c base A or G	c base C or T	c base A or G	c base A or G	base A or G	t c	c base C or T	c base C or T	c base G or T	base A or G	c base A or G	c base G or C	c base C or T	base A or G	c base G or C	c base C or T	c base A or G	c base A or G
: deletion of	: variable m	: polymorphic	: insertion	: polymorphic	: polymorphic	: polymorphic	: polymorphic	: polymorphic	: polymorphic	: polymorphic	: deletion of	: polymorphic	: polymorphic	: polymorphic	: polymorphic	: polymorphic	: polymorphic	: polymorphic	: polymorphic	: polymorphic	: polymorphic	: polymorphic	: polymorphic
10-509-295	10-510-173	10-511-62	10-511-337	10-512-36	10-512-318	10-513-250	10-513-262	10-513-352	.10-513-365	12-206-81	10-343-231	12-206-366	10-343-278	10-343-339	10-346-23	10-346-141	10-346-263	10-346-305	10-347-74	10-347-111	10-347-165	10-347-203	10-347-220
足	P	Ò	LOCATION: 2323 OTHER INFORMATION: NAME/KEY: allele		ORMA	o	o	OTHER INFORMATION: NAME/KEY: allele	9		Ď	Ö	ORMA		COCATION: 5903 OTHER INFORMATION: NAME/KEY: allele	o	OTHER INFORMATION: NAME/KEY: allele	9	o	Ç	Ų.	0	OTHER INFORMATION:

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CAAGAAGCTCTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAAGTTAAATTTAAAT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : polymorphic base A or C
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                 or
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                                                                                                                 : polymorphic base A or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGITITITATGAATAAATTTTAATTGTTGTTTTGCTAGCCT 252
              : polymorphic base A
                                                               : polymorphic base A
                                                                                                                                                                                                                                                                                                                                                                        : polymorphic base G
                                                                                                                                                                                                                                                                                                                                                                                                                             : polymorphic base C
                                                                                                                                                                   : polymorphic base C
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llarity 52.9%; Pred. No. 0.67; '
Conservative 0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                          : deletion of CTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 288, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
PAPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
LOCATION: 6534
OTHER INFORMATION: 10-347-271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 13524
OTHER INFORMATION: 10-507-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: 10-507-321
NAME/KEY: allele
LOCATION: 13524
                               NAME/KEY: allele
LOCATION: 6611
OTHER INFORMATION: 10-347-348
                                                                                                                                                                                                                                                                      OTHER INFORMATION: 10-349-142
                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: 10-349-216
                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 8926
OTHER INFORMATION: 10-349-368
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 12429
OTHER INFORMATION: 10-350-332
                                                                                                               10-348-391
                                                                                                                                                                                                                                                                                                                                                        LOCATION: 8785
OTHER INFORMATION: 10-349-224
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 13341
OTHER INFORMATION: 10-507-170
                                                                                                                                                 LOCATION: 8608
OTHER INFORMATION: 10-349-47
NAME/KEY: allele
                                                                                                                                                                                                     LOCATION: 8658
OTHER INFORMATION: 10-349-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 12171
OTHER INFORMATION: 10-350-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 118; Conserve
                                                                               NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 8777
                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 8703
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LOCATION: 13492
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LOCATION: 13535
                                                                                                                                 NAME/KEY: allele
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US-08-998-416-288
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us-09-508-487-20.rni

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ACCTTTTTTAAATTTCATTAATATGTTACTATAATAACCAGTTTTAATAAAGAGGTTTTTA 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 TAATAAACTTAAT--AATCTATTTATTAATAAAAATGGTATATTTAATATTAAAATTAAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 AAATAAAGACATTATTAAAAGAATTGAAATTGCTAATTTTATGGTCAAATCAAGGTC 99
                                                                                                                                                                                                                     APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.1%; Score 44; DB 4; Length 854; 50.4%; Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
    PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cormualls Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                       Sequence 534, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                  Philippsen, Peter
Pohlmann, Rainer
                                                                                                                                                                                                                                                                                                                                                               1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 854 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Res
STATE: No
COUNTRY:
                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 TTAAATAG-TTTTAAAAACCTTTTTTAAATTTCATTAATATGTTACTATAATACCAGTTT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCTAGCTTTGCTCAAGCTGATGATTCTAAAAGCGCTTTTAATTTGGGAGCGGGGAAAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 TTATTAATATTTATATAATTATAAAATAATATTTAATATGAATACTATTTAGTCTATGT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  405 CTATTTTTATAAATATTATGTTGATTTATATTTAATCTTTTATAAGAATTATTAT 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTITITAGCTIATGAAACTAGTAAGAAAGATCCTATTGTGCCATTTTTATTGAACCTTTT
                            APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.1%; Score 44; DB 4; Length 837
46.0%; Pred. No. 0.4;
tive 0; Mismatches 215; Indels
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 TTTAGGGTTTGGAATAGGTTCTTTTGCTCAAGGAGATATT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
                                                                                                                                                      SSEE: No. 6239264artis Corporation
T: 3054 Cornwallis Road
Research Triangle Park
R: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PREJECTION DATA:
PREJECTION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241
Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 288: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 837 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 46.09
Matches 184; Conservative
                                                                                                                                     CORRESPONDENCE ADDRESS: ADDRESSE: NO. 62392
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: PAG1241RP
US-08-998-416-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                        27709
                                                                                                                                                                                                                   STATE: No COUNTRY:
                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345
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RESULT 14
US-08-617-860B-32/C
Sequence 32, Application US/08617860B
Patent No. 613366
GENERAL INFORMATION:
APPLICANT: Typfer, R., Bautor, J., Bothmann, H., Filsak, E., APPLICANT: HYLICK-GTRANGHORTE, C., Klein, B., Martini, N., APPLICANT: M. 1ler, A., Schulte, W., Voetz, M., Walek, J., TTLLE OF INVENTION: Promoters
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steinberg, Raskin & Davidson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

SOFTWARE: PALENTIN Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/617,860B

FILING DATE: 01-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP94/02950

FILING DATE: 05-SEP-1994

APPLICATION NUMBER: D432951.2

FILING DATE: 04-SEP-1993

INFORMATION FOR SED ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 1850 Base pairs

TYPE: Nucleic acid

STRANDEDNESS: Double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                        CALF: 1.000
COMPOTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OBFRATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                       STREET: 1140 Avenue of the Americas CITY: New York
                                                                         280 CTGATGATTCTAAAAGCGCTTTTAAT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: genomic Lambda FIX II
CLONE: ClTEg1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription start
1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Cuphea lanceolata IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATA-Signal
1553..1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
1797..1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAT-Signal
1428..1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leguminbox
1642..1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Startcodon
1797..1799
                                                                                                                                                                                                                                                                                                                                                                                               New York
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Cup
                                                                                                                                                                                                                                                                                                                                                                                                                                  10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-617-8608-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
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LOCATION:
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FEATURE:
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414 TITICAATATICAAAAATICAAAAATATITAAAAACTITIAAATATATITITAAAACC 355
                                                                                                                                                                       92 AGAAGCTCTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAAGTTAAAATTAAATAG 151
                                                                                                                                                                                                                                                       152 TTTTAAAAACCTTTTTAAATTTCATTAATATGTTACTATAATACCAGTTTTAATAAGA 211
                                               3; Gaps
                                                                                      32 TTTTCGACAAATAAAGACATTATTAAAAGAATTGAAATTGCTAATTTTATGGTCAAATCA 91
Score 44; DB 3; Length 1850;
Pred. No. 0.46;
0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lundberg, Woessner & Kluth, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Topfer, R.
APPLICANT: Martini, N.
APPLICANT: Schell, J.
TITLE OF INVENTION: MEDIUM CHAIN-SPECIFIC THIOESTERS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESSE: Schwegman, Lundberg, Woessner & Kluth, E
                                                                                                                                                                                                                                                                                                                                       212 GGTTTTTATGAATATTTTTAATTGTTT 243
                                                                                                                                                                                                                                                                                                                                                                              237 TTAAAATATATTTAAATTTTAAAAATATTTT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235.001US1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/605,106
FILING DATE: 23-SEPT-1996
FILING DATE: 300
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02935
FILING DATE: 01-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: genomic Lambda FIX II CLONE: ClTEg1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08605106 Patent No. 5910631 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid_
EDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: : DNS (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
LIBRARY: genomin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
      5.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 4098 Base pairs
                                             Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Schwegman,
STREET: P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-605-106-4/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
      Query Match
                          Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
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..3303, 3391..3459, 3672..3941)
                                                                                                                                                                                                                                                                                                                                                                                                                   intron V
3304..3390
                                                         Startcodon
1797..1799
                                                                                                    exon II
1787..2294
                                                                                                                                                intron II
2295..2657
                                                                                                                                                                                             exon III
2658..2791
                                                                                                                                                                                                                                       intron III
2792..2897
                                                                                                                                                                                                                                                                                  exon IV
2898..3011
                                                                                                                                                                                                                                                                                                                              intron IV
3012..3131
                                                                                                                                                                                                                                                                                                                                                                         exon V
3132..3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon VI
3391..3459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron VI
3460..3671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon VII
3672..3941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stopcodon
3942..3944
                                                                                                                                                                                                                              FEATURE:

NAME/KEY:

LOCATION: 2792..

FEATURE:

NAME/KEY: exon

LOCATION: 3012

FEATURE:

NAME/KEY: intro

LOCATION: 3132

FEATURE:

NAME/KEY: intro

LOCATION: 330

FEATURE:

NAME/KEY: intro

LOCATION: 330

FEATURE:

NAME/KEY: intro

LOCATION: 334

FEATURE:

NAME/KEY: intro

LOCATION: 334

FEATURE:

NAME/KEY: e

LOCATION: 34

FEATURE:

NAME/KEY: e

LOCATION: 3

LOCATION: 3

FEATURE:

NAME/KEY: e

LOCATION: 3

LOCATION: 3

LOCATION: 3

LOCATION: 3
            LOCATION:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
LOCATION:
NAME/KEY:
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1; Query Match 5.1%; Score 44; DB 2; Length 4098; Best Local Similarity 53.8%; Pred. No. 0.54; Matches 114; Conservative 0; Mismatches 95; Indels δ a

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Search completed: March 15, 2003, 07:44:04 Job time: 71.8253 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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nucleic search, using sw model

OM nucleic -

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; Search time 1448.7 Seconds
(without alignments)
12999.061 Million cell updates/sec
  March 14, 2003, 20:15:46
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1 tagaattttcaacaaataaa.....atttatctagaaaatgggtg IDENTITY_NUC Gapop 10.0 , Gapext 1.0 US-09-508-487-22 Scoring table: Perfect score: Sequence:

749

49582208 Total number of hits satisfying chosen parameters:

24791104 segs, 12571243825 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ptodata/1/pna/US6039_COMB.seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 22, Appl	Sequence 22, Appl	Sequence 22, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 18, Appl		Sequence 18, Appl	Sequence 63, Appl	Sequence 63, Appl	Sequence 14, Appl	Sequence 14, Appl	Sequence 19, Appl		Sequence 251, App	Sequence 57521		Sequence 57521, A	3 Sequence 57873, A	Sequence 49195, A
SUMMARIES	US-09-153-447-22	US-09-156-447-22	US-09-508-487-22	US-09-153-447-20	US-09-156-447-20	US-09-508-487-20	US-09-153-447-18	US-09-156-447-18	US-09-508-487-18	PCT-US98-12764-63	US-09-830-228-63	PCT-US98-12764-14	US-09-830-228-14	PCT-US98-12764-19	US-09-830-228-19	US-10-221-613-251	US-09-362-510-57521	US-09-362-510A-57521	US-09-904-013-57521	US-09-873-402A-57873	US-60-209-830-49195
DB	15	15	19	15	15	19	15	15	19	Н	32	Н	32	Н	32	42	17	17	34	33	64
% Query Match Length DB	749	749	749	862	862	862	759	759	759	1761	1761	9399	9399	7074	7074	7110	417	417	417	402	402
% Query Match	100.0	100.0	100.0	81.0	81.0	81.0	74.5	74.5	74.5	13.1	13.1	12.2	12.2	11.0	11.0	8.8	8.2	8.2	8.2	7.9	7.9
Score	749	749	749	607	607	607	558.2	558.2	558.2	98.4	98.4	91.6	91.6	82.2	82.2	99	61.4	61.4	61.4	59.4	59.4
Result No.	1	7	9	4	2	9	7	œ	6	c 10	c 11	12	13	14	15	16	c 17	c 18	c 19	c 20	c 21

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/ptodata/1/pna/US100A_COMB.seq:* /ptodata/1/pna/US10B_COMB.seq:* /ptodata/1/pna/US101A_COMB.seq:* /ptodata/1/pna/US101B_COMB.seq:*

/cgn2_6/ptodata/1/pna/US102B_COMB.seg:

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; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	GAAAAAGTTAAATTTA 120
9-821-837-2899 9-304-517A-2679 9-504-517A-2679 9-555-240-5262 9-654-617-7176 9-684-016-7176 9-684-016-7176 9-684-016-7256 9-684-016-7256 9-684-016-7256 9-684-016-7256 9-684-016-7256 9-684-016-7256 9-684-016-7256 9-684-016-7256 9-684-016-7256 9-684-016-7256 9-684-016-7256 9-688-2437 9-688-888-888-8933 9-685-439-4003 9-688-888-888-8933 9-685-439-4003 100 No. 4.4e-122 150 NEELIA 1018-128-128-128-128-128-128-128-128-128-1	GAGTAACAATTT
22 58.8 7.9 588 31 US-09- 24 58 7.7 353 17 US-09- 25 58 7.7 353 17 US-09- 26 58 7.7 353 27 US-09- 27 58 7.7 353 27 US-09- 28 57.2 7.6 472 25 US-09- 31 57 7.6 472 25 US-09- 32 56.8 7.6 472 25 US-09- 33 56.8 7.6 195257 66 US-09- 34 56.8 7.6 195257 67 US-09- 35 56.8 7.6 195257 67 US-09- 36 56.6 7.6 9021 41 US-10- 37 7.6 472 63 US-09- 38 56.8 7.6 195257 67 US-09- 39 56.2 7.5 633 33 US-09- 44 55.8 7.6 19257 75 US-09- 45 56.6 7.5 1938 04 2 US-10- 44 55.8 7.4 14147 41 US-10- 44 55.4 7.4 14147 41 US-10- 45 54.6 7.3 391 33 US-09- 46 55.2 7.5 633 33 US-09- 47 55.4 7.4 14147 41 US-10- 48 55.4 7.4 14147 41 US-10- 49 55.4 7.4 14147 41 US-10- 40 55.2 7.5 633 33 US-09- 45 54.6 7.3 391 33 US-09- 45 54.6 7.3 391 33 US-09- 46 55.2 7.5 630 35 US-00- 47 55.4 7.4 14147 41 US-10- 48 55.4 7.4 14147 41 US-10- 49 55.2 7.5 63 33 33 US-09- 40 55.2 7.5 63 33 33 US-09- 40 55.2 7.5 63 33 33 US-09- 41 55.8 7.6 7.3 391 33 US-09- 42 55.4 7.4 14147 41 US-10- 44 55.8 7.3 391 33 US-09- 45 54.6 7.3 391 33 US-09- 45 54.6 7.3 391 33 US-09- 45 54.6 7.3 391 33 US-09- 45 54.6 7.3 391 33 US-09- 46 55.2 7.5 63 33 33 US-09- 47 55.4 7.4 14147 41 US-10- 48 55.4 7.4 14147 41 US-10- 48 56.5 80 TWARE: EACHIEN VET. 2.1 SOUTHARRY ETLING DATE: 1997-09-10 EARLIER FILING DATE: 1997-09-10 EARLIE	ANCAGAAGCTCTAITGGTAAGCGAAITTC
22 23 23 24 25 26 27 28 30 31 31 31 31 31 31 31 31 31 31 31 31 31	Oy 61 AATCA Db 61 AATCA OY 121 AATAG OY 121 AATAG OY 181 AAGGG OY 181 AAGGG

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                     OM nucleic - nucleic search, using sw model
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Run. on:

March 14, 2003, 22:48:52; search time 48.9852 Seconds (without alignments) 10731.744 Million cell updates/sec

US-09-508-487-22 749 1 tagaattttcaacaaataaa.....atttatctagaaaatgggtg 749 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

501302 seqs, 350932545 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published_Applications_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			æ				
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. 0	-	52	6.9	416	10	US-09-960-352-4584	Sequence 4584, Ap
	7	48.4	6.5	416	10	US-09-960-352-4584	Sequence 4584, Ap
	e	48.2	6.4	2000	σ	US-09-938-842A-5004	Sequence 5004, Ap
	4	48	6.4	1044	σ	US-09-998-059-10	Sequence 10, Appl
	2	48	6.4	1051	σ	US-09-998-059-22	22,
	9	48	6.4	1140	6	US-09-998-059-29	Sequence 29, Appl
U	7	47.2	6.3	640681	10	US-09-790-988-1	
	8	46.8	6.2	2251	10	US-09-796-256A-11	11,
	σ	45.8	6.1	385	10	US-09-960-352-1739	-
_	9	45.8	6.1	419	10	US-09-960-352-11234	Sequence 11234, A
c o	-	45.2	6.0	3272	10	US-09-796-348-18	
~	2	44.2	5.9	376	10	US-09-960-352-5087	
7	<u></u>	44.2	5.9	640681	10	US-09-790-988-1	Sequence 1, Appli
c J	4	44	5.9	513509	σ	US-09-754-853A-4	Sequence 4, Appli
-	5	43.8	5.8	516	10	US-09-960-352-5785	Sequence 5785; Ap
7	9	43.4	5.8	397	10	US-09-960-352-13784	Sequence 13784, A
0	2	43.4	5.8	411	10	US-09-960-352-14521	Sequence 14521, A
_	89	43.4	5.8	413	10	US-09-960-352-2919	Sequence 2919, Ap
_	61	43.4	5.8	431	10	US-09-960-352-5558	Sequence 5558, Ap

Sequence 2, Appli Sequence 3, Appli Sequence 12872, A	Sequence 4999, Ap Sequence 135, App	Sequence 3400, Ap Sequence 2, Appli	Sequence 3, Appli Sequence 2412, Ap	Sequence 2276, Ap	Sequence 13489, A	Sequence 3, Appli	Sequence 3655, Ap Sequence 5073, Ap	Sequence 1, Appli	П	Sequence 2699, Ap	Sequence 47, Appl	Sequence 9, App	Sequence 13, A	Sequence 19, Appr	Sequence 17, Appl	Sequence 4, Appli	Sequence 11, Appl	Sequence 3371, Ap	Sequence 30, Appl
9 US-09-754-853A-2 9 US-09-754-853A-3 10 US-09-960-352-12872	9 US-09-938-842A-4999 9 US-10-098-841-135	10 US-09-960-352-3400 9 US-09-754-853A-2	9 US-09-754-853A-3 10 US-09-960-352-2412	10 US-09-954-456-2276	10 US-09-960-352-13489	10 US-09-820-905-3	9 US-09-938-842A-3655 9 US-09-938-842A-5073	10 US-09-816-028A-1	10 US-09-960-352-1243	10 US-09-960-352-2699	10 US-09-834-975-47	10 US-09-770-149-9	10 US-09-725-735A-13	10 US-09-796-348-19	10 US-09-796-348-17	9 US-09-754-853A-4	10 US-09-796-256A-11	10 US-09-960-352-3371	10 US-09-804-682-30
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5.8	5.7	5.7	5.7	5.7	5.7	5.7	o r	5.6	5.6	5.6	5.6	5.6	5.6	5.5	5.5	5.5	5.5	5.5	5.5
43.4	443	42.8 42.8	42,8	42.6	42.4	42.4	2.4	41.8	41.6	41.6	41.6	41.6	41.6	41.4	41.4	41.4	41.2	41	41
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ALIGNMENTS

RESULT 1 US-09-96 Sequen Sequen GENERA APPLI APPLI TITLE TITLE TITLE TITLE TITLE TITLE SCURRE CURRE CURRE SEQ IDE SEQ IDE LENG LENG LENG CORRE C	RESULT 1 US-09-060-352-4584/C Sequence 4584, Application US/09960352 Sequence 4584, Application US/09960352 Sequence 4584, Application US/09960352 Sequence 4584, Application US/09960352 GENERAL INFORMATION: APPLICANT: Warren, Wesley C. APPLICANT: Byart, John C. APPLICANT: Byart, John C. APPLICANT: Byart, John C. TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION TITLE OF SEQ ID NOS: 15112 SEQ ID NO 4584 TYPE: DAM ORGANISM: Bos tautus OTHER INFORMATION: Clone ID: 20-LIB3057-016-01-K1-E11
Query	Query Match 6.9%; Score 52; DB 10; Length 416;
Best L	Best Local Similarity 51.8%; Pred. No. 0.29;
Matche	Matches 118; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
Qy 9	95 taacaatttgaaaaagttaaatttaaatacttccaaaagccttttttaaatttcattaa 154
Db 28	
Qy 15	155 TATGCTACCATAATACCAGTTTAAAAGGGGTTTTTATGAATAAGTTTTTAATTTTTAT 214
Db 22	
Oy 21	215 ITIGGIAAICITITGGCTITITCIAGITITGCICAAGAIGAITCIAAAAGCACITITAA 274
Db 16	
Qy 27	275 TCTGGGAGCGGAGAAAATTTTGGTTTATGAAACTAATAAGAAGA 322
Db 10	

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186 AGTACTATCATTAGTAAAATCTCTCGAATATAATATATGATTGCAAAAATATCACATTA 245
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                                                                                                                                62 ATCAAGAAGCTCTATTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAAGTTAAATTTAA
                                                                                                                                                                                                                                                                                                                  180 AAAGGGGTTTTTATGAATAAGTTTTTAATTTTTAGTAATCTTTTGTGCTTTTTCT
                                            2 AGAATITICAACAAATAAAGATATIGITAAAAGAATIGAAATIGCTAATITIATGGTTAA
                                                                                                                                                                                                                         122 ATAGTTCCAAAAGCCTTTTTTAAATTTCA--TTAATATGCTACCATAATACCAGTTTAAT
0; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09998059
Publication No. US2003005485A1
GENERAL INFORMATION:
APPLICANT: Ohlrogge, John B.
APPLICANT: Gao, Hongbo
APPLICANT: Grie, Thomas
APPLICANT: Grie, Thomas
APPLICANT: Grie, Thomas
APPLICANT: White, Joseph A.
TITLE OF INVENTION: Plant Seed Specific Promoters
FILE REFERENCE: MSU-06689
CURRENT APPLICATION NUMBER: US/09/998,059
CURRENT FILING DATE: 2001-11-30
PRIOR PILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
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US-09-998-059-22
'Sequence 22, Application US/09998059
'Publication No. US20030005485A1
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                          240 AGTITIGCICAAGAIGATI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 TTGTAGGATCATGTAAATT 444
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Best Local Similarity 51.4%;
Matches 111; Conservative
Matches 134; Conservative
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US-09-998-059-10
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APPLICANT: Mang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPRESENCE: SCREPIAGO.3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT PILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR PRIOR PLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-01-16
PRIOR PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 5004
                                                        Sequence 4584, Application US/09960352
Patent No. US20201313391
Patent No. US20201313391
GENERAL INFORMATION:
APPLICANT: Wasten, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILLE REFERENCE: 16511.006/37-21(10299)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 4584
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                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
: ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB3057-016-Q1-K1-E11
US-09-960-352-4584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.5%; Score 48.4; DB 10;
Best Local Similarity 51.4%; Pred. No. 1.3;
Matches 112; Conservative 0; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 TATGAATAAGTTTTTAATTTTTATTTTGGTAATCTTTT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5004, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
APPLICANT: Harper, Jeff
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Best Local Similarity
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                                     US-09-960-352-4584
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90 TCGAGTAACAATTTGAAAAAAGTTAAAATTTAAATAGTTCCAAAAGCCTTTTTAAATTTC 149 624 TIAAAITCITAITIATAAACATAAAGIAAITITTAATITICITIAAITAAAAATACATAI 683 30 AAAAGAATTGAAATTGCTAATTTTATGGTTAAATCAAGAAGCTCTATTGGTAAGCGAATT 504 ATATGAATGCTATTTTTGTCTTAAAAACTTAAAAATTGTACTATTTGAAGGAATTTCATTT 150 ATTAATATGCTACCATAATACCAGTTTAATAAAGGGGTTTTTATGAATAAGTTTTAATT DB 9; Length 1044; 105; Indels 210 TTTATTTTGGTAATCTTTTGTGCTTTTTCTAGTTTT 245 Pred. No. 1.8; 0; Mismatches Score 48;

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Pred. No. 6;
0; Mismatches 123;
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                                                                                                                            TITATITIGGIAAICITITIGIGCTITITICIAGITIT 245
                                                                                                                                               Sequence 11, Application US/09796256A Patent No. US20020078477A1 GENERAL INFORMATION: APPLICANT: Chiang, Vincent L
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; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
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Best Local Similarity 51.5%;
Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
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Pred. No. 1.8;
0; Mismatches 105; Indels
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                                 APPLICANT: Gao, Hongbo
APPLICANT: Glrke, Thomas
APPLICANT: Glrke, Thomas
APPLICANT: White, Joseph A.
TITLE OF INVENTION: Plant Seed Specific Promoters
FILE REFERENCE: MSU-06689
CURRENT APPLICATION NUMBER: US/09/998,059
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/250,401
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 60
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APPLICANT: Girke, Thomas
APPLICANT: White, Joseph A.
TITLE OF INVENTION: Plant Seed Specific Promoters
FILE REPERENCE: MSU-06689
CURRENT APPLICATION NUMBER: US/09/998,059
CURRENT FILING DATE: 2001-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 TTTATTTTGGTAATCTTTTGTGCTTTTTCTAGTTTT 245
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PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
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Publication No. US20030005485A1
GENERAL INFORMATION
APPLICANT: Ohlrogge, John B.
APPLICANT: Benning, Christoph
                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-998-059-22
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Ohlrogge, John B.
Benning, Christoph
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SEQ ID NO 22
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Best Local Similarity 51.4%;
Matches 111; Conservative
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Matches 111; Conserv
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546384 GTAATITITTAATATITTAATATITGATGCGATCTATITGAATITCCATITITAATAT 546325
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ATTAATATGCTACCATAATACCAGTTTAATAAAGGGGTTTTTATGAATAAGTTTTTAATT 209
                                                          677 ттаааттсттаттатаасатааастаататттаатттстттааттаааатасатат 736
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PEPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617/c-3532.0
CURRENT APPLICATION NUMBER: US/09/796,256A
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US60/033381
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: HATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILLE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
PRIOR APPLICATION NUMBER: J2000-04-07
NUMBER OF SEQ ID NOS: 7
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID BAD OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/09796348
Patent No. US20020048757A1
GENERAL INFORMATION:
APPLICANT: MAIL, Katsumi
APPLICANT: GAMOU, Takuma
TITLE OF INVENTION: A SIMPLE AND QUICK METHOD FOR DETERMINING THE NUCLEOTIDE SEQUETILE OF INVENTION: A SIMPLE AND QUICK METHOD FOR DETERMINING THE NUCLEOTIDE SEQUETILE OF INVENTION: AITOCHONDRIAL 21S RIBOSOMAL RNA GENE OF YEAST BELONGING TO SATITLE OF INVENTION: CEREVISIAE
FILE REFERENCE: 1254-0171P
CURRENT FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 ITCTAAAAGCACTTTTAATCTGGGAGCGGGAGAAAATTTTTGGTTTATGAAACTAATAA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 TITITIAAATITCATTAATAIGCTACCATAATACCAGTTTAATAAAGGGGTTTTATGAA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 TTAAAAATTATAAAAAAATTTTTAAAAAGTTAAAAATTTTATAATTTTAAAATATAAAA 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 GAAAGATTCTCTTGTACCATTTTTATTGAACCTTTTTTAGGGTT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INCEMATION: CLone ID: 48-LIB3058-052-Q1-K1-D8
US-09-960-352-11234
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45.0%; Pred. No. 6.8;
tive 0; Mismatches 208;
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Pred. No. 4;
                                                                                                                                                                                                 Sequence 11234, Application US/09960352 Patent No. US20020137139A1
                                 TTTAGGGTTCGGGATAGGTTCTTTT 377
                                                                             360 GTTTTTTTTTTTTTTTTTTTT 384
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; ORGANISM: Saccharomyces cerevisiae
US-09-796-348-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.1%;
                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 50.2
Matches 113; Conservative
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Mengbing
APPLICANT: Tao, Mengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID ADD OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 GTTTAATAAAGGGGTTTTTATGAATAAGTTTTTAATTTTTATTTTGGTAATCTTTTGTGC 232
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ORGANISM: Bos taurus
CTHER INFORMATION: Clone ID: 08-LIB3058-031-Q1-K1-B7
US-09-960-352-1739
                                                                                                                                                                                                                                                                                                              92;
                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.1%; Score 45.8; DB 10;
48.3%; Pred. No. 3.9;
tive 0; Mismatches 137;
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Pred. No. 3.3;
0; Mismatches
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PRIOR FILING DATE: 1996-12-16
PRIOR APPLICATION NUMBER: 08/991677
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                              Query Match 6.2%;
Best Local Similarity 52.6%;
Matches 102; Conservative
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Best Local Similarity 48.38
Matches 128; Conservative
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                                                                                                                                                                                          ; ORGANISM: Pinus taeda
US-09-796-256A-11
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US-09-960-352-1739
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                                                                                                                                                                       TYPE: DNA
                                                                                                                                              LENGTH:
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Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 640681;
                                                                                                                                                                                        APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: SARAKI, YOSHIYUKI
TITLE OF INVENTION GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-03-23
PRIOR PILING DATE: 2000-04-07
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Pred. No. 21;
0; Mismatches 111; Indels
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APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REPERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
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LOCATION: (111805)..(113968),(114684)..(115204)
FEATURE:
339 TTTTATTTTTTATTTATTTTTTTTATTATT 371
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; Sequence 4, Application US/09754853A
; Publication No. US20030005491A1
; GENERAL INFORMATION:
                                                                                                                             Sequence 1, Application US/09790988 Patent No. US20020127687A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.9%;
Best Local Similarity 52.9%;
Matches 127; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
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                                                                                                                                                                        GENERAL INFORMATION:
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Wasley C.
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5087
LENGTH: 376
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                                                                                                                                             2512 TGTGAACCCCCACCGAGAGGAGAAGTTATTATTGTTTTCCTTACAATTTTACTGTAC 2453
                                                                                                                                                                                                                                                                                                                                                                                                              TITATGGACTIATTCAGATACTITTGCTGATAATGACGCCCCCATCAAAACTACCAATTAG 2273
                                                                                                                                                                                                                                     ATATTTTTATCTATTACTAAAATATATTCAATAAATATAAATTTATATAAACATATTTCA 2393
                    TAAAATTTAAAATAGTTCCAAAAGCCTTTTTTAAATTTCATTAATATGCTACCATAATACCA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 TGGATTTGATGCGGTTGGTATAGGGTTAATACTTACAGGAGCTTATTTGGACATCAAGGA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 TAATATTTTTTATTAATTTACATTTTTAATTATTTTTAATATTTTCATTTAAAT 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 TITITAATITITATITIGGTAATCITITIGGCTTTTTCTAGTTTTGCTCAAGATGATTCT 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 TITITIAATITITITITITITITATTATTITAATITITITITITITITITITITITATTITITAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 GATTCTCTTGTACCATTTTTATTGAACCTTTTTTAGGGTTCGGGATAGGTTCTTTTGCT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 ATTITIGGTTTATGAAACTAATAAGAAAGATTCTCTTGTACCATTTTTATTGAACCTTTT
                                                                                                                                                                                                                                                                                                                                                                     TITAGGGTTCGGGATAGGTTCTTTTGCTCAAGGAGATATCCTTGGAGGTTCTCTTATTCT
                                                                                                                                                                                        233 TTTTTCTAGTTTTGCTCAAGATGATTCTAAAAGCACTTTTAATCTGGGAGCGGGAAAA
                                                                                                      GTTTAATAAAGGGGTTTTTATGAATAAGTTTTTAATTTTTATTTTGTGCTAATCTTTTGTGC
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; OTHER INFORMATION: Clone ID: 22-LIB3058-032-Q1-K1-F9
US-09-960-352-5087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44.2; DB 10;
Pred. No. 7.7;
0; Mismatches 143;
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US-09-960-352-5087
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Best Local Simi
Matches 130;
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: Mathialagan, Magapan
TITLE OF INVENTION: MUSCLEC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5785
LEWITH: 516
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                                                                                                                                                                                                                                                                          Db 110156 TTTACATCAAATTAAATCTGTTTACCAAAATAAAAGGAGAGAAATTAGAATTAAAAATTT 110097
                                                                                                                                                                                                                                                                                                                                                              110096 GATGTTTCCTTTTAAAAGAATTACATTGTTAAGTTAATATTTTTGGTTATTAAAGAAAT 110037
                                                                                                                                                                                                                                                                                                                                                                                                                                       187 TTTTTATGAATAAGTTTTTAATTTTTATTTTGGTAATCTTTTGTGCTTTTTCTAGTTTTG 246
                                                                                                                                                                                                                                                                                                                      67 GAAGCTCTATTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAAAGTTAAAATTTAAAATAGT 126
                                                                                                                                                                                                                                                                                                                                                                                                              127 TCCAAAAGCCTTTTTTAAATTTCATTAATATGCTACCATAATACCAGTTTAATAAAGGGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 CTCAAGATGATTCTAAAAGCACTTTTAATCTGGGAGCGGGAGAAAAATTTTTGGTTTATG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 AACAATTTGAAAAAAGTTAAAATTTAAATAGTTCCAAAAGCCTTTTTTAAATTTCATTAAT 155
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                                                                                                                                                                                                                             7 TITCAACAAATAAAGATATTGTTAAAAGAATTGAAATTGCTAATTTTATGGTTAAATCAA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 ATTACAATTIGITTATAGAGTTTAAATTCTTAATGGCAATAAGGTATNGAGGGTTAGTTT
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                                                                                                                                   Length 513509
                                                                                                                                      Score 44; DB 9; Length 513
Pred. No. 22;
0; Mismatches 165; Indels
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LOCATION: (76),(90)
OCHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 25-LIB3057-018-Q1-K1-G1
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                  LOCATION: (1)..(513509)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 318013_region_A3
US-09-754-853A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5785, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
                                                                                                                                 Query Match 5.9%;
Best Local Similarity 46.4%;
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 43.89
Matches 186; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 AAACTAAT 314
NAME/KEY: unsure
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US-09-960-352-5785
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215
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                                                216 TIGGTAATCTTTTGTGCTTTTTCTAGTTTTGCTCAAGATGATTCTAAAAGCACTTTTAAT
                                                                                              336 ITTTTATIGAACCTTTTTTAGGGTTCGGGATAGGTTCTTTTGCTCAAGGAGATATCCTT
                                                                                                                            396 GGAGGTTCTCTTATTCTTGGATTTGATGCGGTTGGTATAGGGTTAATACTTACAGGAGCT
                                                                                                                                                                156 ATGCTACCATAATACCAGTTTAATAAAGGGGTTTTTATGAATAAGTTTTTAATTTTTATT
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Search completed: March 15, 2003, 14:38:36 Job time: 1077.99 secs

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us-09-508-487-21 rapn
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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 14:25:06; Search time 23 Seconds (without alignments)

1006.876 Million cell updates/sec

Perfect score: US-09-508-487-21
Sequence: 1 MNKFLIVVLLAFCVFSSFAQ.......DINMGQASALGFELSFKKSY 178

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 598297 seqs, 130101922 residues

Total number of hits satisfying chosen parameters: 598297
```

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/USOG_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USOG_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 69822, A	Sequence 5340, Ap		57091,		•		48,	Sequence 42, Appl		Sequence 11883, A			Sequence 78114, A		Sequence 332, App			-	133;	٠.	Sequence 23305, A	Sequence 9442, Ap	19854,	Sequence 19854, A	
ΩI	US-10-282-122A-69822	US-09-134-000C-5340	US-09-134-000C-5340	US-10-282-122A-57091	US-10-369-493-12272	US-10-282-122A-73910	US-10-282-122A-71751	US-10-369-493-48	US-10-354-774-42	US-09-988-067B-6	US-10-156-761-11883	US-10-282-122A-51378	US-10-366-683-19571	US-10-282-122A-78114	US-10-282-122A-66257	US-10-287-274-332	US-10-282-122A-56452	US-10-282-122A-75460	US-10-354-774-40	US-10-156-761-13326	US-10-282-122A-53673	US-10-369-493-23305	US-10-156-761-9442	PCT-US02-32727-19854	US-09-978-825-19854	US-10-057-498-19854
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% Query Match	9.6	9.6	9.6	9.6	9.5	9.5	9.5	0.6	9.0	0.6	9.0	9.0	8.7	8.7	8.7	8.7	8.7	8.7	8.7	9.8	8.5	8.5	8.5	8.5	8.5	8.5
Score	89.5	87	87	87	83.5	83.5	83	81.5	81.5	81	81	81	79	78.5	78.5	78.5	78.5	78.5	78.5	78	77	77	77	76.5	76.5	76.5
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Sequence	edneuce	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
JS-10-282-122A-73132	75-09-950-084-6659	JS-10-282-122A-4444	US-10-369-493-1078	US-10-282-122A-59036	JS-10-369-493-6417	US-10-369-493-11538	US-09-134-000C-6426	US-09-134-000C-6426	JS-10-366-683-19270	US-10-282-122A-49274	US-10-282-122A-78316	JS-10-282-122A-50724	JS-10-156-761-12262	JS-10-282-122A-59641	JS-10-156-761-10352	JS-10-282-122A-72971	JS-10-282-122A-44555	JS-10-282-122A-52786
9.	<u> </u>	_	9		9	9	2	2	9	9	9	9	9	9	9	9	9	9
652	703	466	1226	206	389	375	499	499	542	214	429	203	403	409	470	479	561	337
8.5	4.4	8.4	8.4	8.4	8.4	8.3	8.3	8.3	8.3	8.2	8.2	8.2	8.2	8.2	8.2	8.2	8.2	8.1
76.5	0	9/	92	75.5	75.5	75	7.5	75	75	74.5	74.5	74	74	74	74	74	74	73.5
. 27	97	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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18-91-03-8-120A-698122

18-940ance 688122, Application US/1028112A

18-940ance 688122, Application US/1028112A

18-940ance 688122, Application US/1028112A

18-94DLICANY: Mandy Liangsu

18-94DLICANY: Mascalbeck, Robert

18-94DLICANY: Mascalbeck, Robert

18-94DLICANY: Mascalbeck, Robert

18-94DLICANY: Mascalbeck, Robert

18-94DLICANY: Trawick, John

18-94DLICANY: Trawick, John

18-94DLICANY: Trawick, John

18-94DLICANY: Trawick, John

18-94DLICANY: Rorsyth, H.

18-94DLICANY: Numbers: Gold-220

18-94DLICANY: Numbers: Gold-220

18-94DLICANY: Numbers: Gold-220

18-94DLICANY: Numbers: Gold-32-31

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18-94DLICANY: Numbers: Gold-32-31

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18-94DLICANY: Numbers: Gold-32-32

18-94DLICANY: Numbers: Gold-32-33

18-94DLICANY:
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10-282-122A-57091
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERCOCCUGS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR PILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5340, Application US/09134000C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 03796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
                                                                                                                     49 MVIAPIIFCTVVSGIAGMQNMKSVGKTGGYALLYFELVSTIALLIGLIVVNVVQPGAGMN 108
                                                                                                                                                                                                            109 IDVSTLDASKIAAYVTAGKDQSIVGFILNVIPNTIVGAFANGDIL---QVLMFSVIFGFA 165
                                                                                                                                                                                                                                                                 84 LILTGAY----LD------IKALDKNAPKAAFKWTWGKGMMLAGAV-TMAVTRL 126
                                                                                                                                                                                                                                                                                                             166 LHRLGSYGKPVLDFIDRFAHVMFNIINMIMKLAPIGAF----GAMAFTIGAYGVSSLVQL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...--LFLG------FGIGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 PKAAFKW--TW-----GKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFG- 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 IVALVIYALFPILONTYTGLTEIDPSLEEAAEAFGMSKKEKLFKFELOM---ALPFIISG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 IRTATVLIIGTATLAALIGAGG-----LGTFILLGIDRNNLSLIFIG-----ALSSAA 189
                                                  Gaps
                                                                                                                                                                              -----EKLLAYETSKKD-PIVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAV-GIG 83
                                                                                            --GAG-- 33
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      DB 6; Length 450;
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                                                Indels
                                                                                       5 LIVVLLAFC-VFSSFAQADDSKSA-----FNL----
9.9%; Score 89.5; DE 26.2%; Pred. No. 0.6; Live 22; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Enterococcus faecalis
US-09-134-000C-5340
                                                Conservative
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                       Local Similarity
mes 49; Conserv
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222 GQLMICF 228
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US-09-134-000C-5340
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LENGTH: 505
    Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LFLG------FGIGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 PKAAFKW--TW-----GKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFG- 152
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                                                                                                                                                                                                                                                                                                                                54;
                                                                                                                                                                                                                                                                  9.6%; Score 87; DB 5; Length 505; 23.3%; Pred. No. 1.2; tive 26; Mismatches 68; Indels
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 57091, Application US/10282122A GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR PILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-110-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
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                                                                                                                                                                              Enterococcus faecalis
                           NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 5340
LENGTH: 505
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PRIOR FILING DATE: 1997-08-15
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
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Trawick, John
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244 GAEPDIIINMYKA 256
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Best Local Similarity
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APPLICANT: XU, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A

CURRENT APPLICATION NUMBER: U5/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR PILING DATE: 2000-03-21

PRIOR PLICATION NUMBER: 60/201,727

PRIOR PLICATION NUMBER: 60/207,727

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PLING DATE: 2000-09-06

PRIOR PAPLICATION NUMBER: 60/230,347

PRIOR PLING DATE: 2000-09-09

PRIOR PAPLICATION NUMBER: 60/242,578

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-16

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420 AGALVLAIKKYVKVPRSLEGAKSILLIPLLGTILTGFVMLAVNIPMAAINTAMNDFLGG- 478
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25.3%; Pred. No. 3.9;
tive 22; Mismatches
  Sequence 73910, Application US/10282122A
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; GENERAL INFORMATION:
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                                                                                                                                     Haselbeck, Robert
Ohlsen, Kari
Syskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Mallone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Best Local Similarity 25.34
Matches 39; Conservative
                                                        APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Stater, Coldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
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                                                                                                                                                                        Length 505;
                                                                                                                                                                                                                             68; Indels
                                                                                                                                                                     9.6%; Score 87; DB 6; 23.3%; Pred. No. 1.2;
                                                                                                                                                                                                                             26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 12272, Application US/10369493 ; GENERAL INFORMATION:
                                                  TYPE: PRT; ORGANISM: Enterococcus faecalis
US-10-282-122A-57091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mesorhizobium loti
US-10-369-493-12272
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                                                                                                                                                                                                                             45; Conservative
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                                                                                                                                                                                                   Best Local Similarity
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Matches 51; Conserv
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US-10-282-122A-73910
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US-10-369-493-12272
SEQ ID NO 57091
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                          LENGTH:
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Gaps

39;

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CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thalley, Bruce S.
TITLE OF INVENTION: Multivalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42, Application US/10354774 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Williams, James A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397-8338
                                                                                                                                                                                                                                                            Query Match 9.0%;
Best Local Similarity 24.6%;
Matches 44; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 39 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                      ; ORGANISM: Aquifex aeolicus US-10-369-493-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-354-774-42
                                                                                                                  SEQ ID NO 48
LENGTH: 692
                                                                                                                                                                     TYPE: PRT
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                             APPLICANT: Forsyth, R. APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 APKAAFK--WTWGKGMMLAGAVTMAVTRLTEI-----IIPF-----TFAN---- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 LQKLGAKKPLLVGSGFAFLGLLLSLTFLPNVAYIISSIIGYLLFGIGLGTYATPSTDTA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 NLFLGFGIGSFAQGDILGGFLI-----LGFDAVGIGLI----LTGAYLDIKALDKN 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LIVVLLAFCVFSSFAQADD-----SKSAFNLGAGEKLLAYETSKKDPIVPFLL--- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior Application data removed - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 ------SYNRKLKNSLNIAFG-----GFEPSF-DINMGQASALGF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 VAEAPDDKVGVASGLYKMASSLGNAFGVAMSSTIYGFGASFMNLQLGGAAGVLF 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Length 464;
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2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.2%; Score 83; DB 23.9%; Pred. No. 2.8; tive 31; Mismatches
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-06
PRIOR PELING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PELING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-10-369-493-48
is Sequence 48, Application US/10369493
is GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
                                                                                            Yamamoto, Robert
                                                                                                                                                                                   FILE REFERENCE: ELITRA.034A
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Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.2
Best Local Similarity 23.9
Matches 56; Conservative
                                              Trawick, John
                        Danie
                                                               Grant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 YVKQRIRVDGWQEDLDAQNQKELMPVKKVLDKEG-----KWLKCYVYVRDEKVYFGVW-- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 GMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASALGF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 YETSKKDPIVPFL-----LNLFLGFGIGSFAQGDILGGFLILGFDAVGIGLILTGA 89
                                                                                                                                                                                                                                                                                  69;
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                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                                                                 Score 81.5; DB 6;
Pred. No. 6.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Botulinum Neurotoxin
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                                                                                                                                                                                                                                                                                  17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/704,159
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America ZIP: 94104
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-354-774-42
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11883
LENGTH: 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 51378, Application US/10282122A
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 ALALGEGVLGMTSAY-TSKREQF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                ; ORGANISM: Streptomyces avermitilis US-10-156-761-11883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-282-122A-51378
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                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                   620 IVPY-IGLALNVG-NETAKGNFENAFELAGASILLEFIPELLIPVVGAFLLESYIDNKNK 677
                                                                                                                                                                                         678 IIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKALNYQAQALEEIIKYR 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AVGIGLI----LTGAYLDIKALDKNAPKAAF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 IVFLPYGFNTDLLINWTNDKRASQKYVERRVKGLSIFYKDMTGRTLDANTL-KKASRHVF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                    -GIGLILTGAYLD---- 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 VFSSFAQADDSKSAFN-LGAGEKLLAYETSKKDPIVPFLLNLFLGF---GIGSFAQGDIL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
                          35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Helicobacter Polypeptides and TITLE OF INVENTION: Helicobacter Polypeptides and TITLE OF INVENTION: Corresponding Polynucleotide Molecules FILE REFERENCE: 06132/04000.

CURRENT APPLICATION NUMBER: US/09/988,067B

CURRENT FILING DATE: 2003-01.31

PRIOR FILING DATE: 1997-04-01

NUMBER OF SEQ ID NOS: 112

SOFTHARE: PastSEQ for Windows Version 4.0

LENGTH: 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 9.0%; Score 81; DB 5; Length 305; 1 Similarity 28.1%; Pred. No. 2.7; 57; Conservative 23; Mismatches 75; Indels
                          56; Indels
  23.8%; Pred. No. 15;
Live 24; Mismatches
                                                                47 IVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAV---
                                                                                                                                                  93 -IKALDKNAPKAAFKWTWGKGMMLAGAVTMAVTRL-
                                                                                                                                                                                                                                    135 FANSYNRKLKNSLNIAFGGFEPSFDINMGQA 165
                                                                                                                                                                                                                                                              Sequence 11883, Application US/10156761 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09988067B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :| :| :| :: :| :| :| DEIYLGGSSVELGVKVPAFKVNY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 -- INMGQASA-LGFEL-SFKKSY 178
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haas, Rainer
APPLICANT: Kleanthous, Harold
APPLICANT: Tomb, Jean-Francois
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Helicobacter pylori
US-09-988-0678-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Al-Garawi, Amal
Odenbreit, Stefan
Meyer, Thomas
Best Local Similarity 23.8%
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 GGFLILGFD------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-10-156-761-11883
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US-09-988-067B-6
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms File REFERENCE: ELITRA-034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                        ---GFPVATFQAVAV 275
                                                                                                                                                                                                                                                                83 GLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRK 142
                                                                                                                                 27 AFNLGAGEKLL----AYETSKKDPIVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAVGI 82
Query Match 9.0%; Score 81; DB 6; Length 379; Best Local Similarity 24.2%; Pred. No. 3.5; Matches 37; Conservative 26; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                               143 LKNSLNIAFGGF--EPSFDINMGQASALGFELS 173
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APPLICANT: Rubenfield, Marc J.
APPLICANT: Rubenfield, Marc J.
APPLICANT: Nolling, Jork
APPLICANT: Deloughery, Craig
APPLICANT: Belsh, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: PATH03-04
CURRENT APPLICATION NUMBER: US/10/366,683
CURRENT FILING DATE: 203-02-13
PRIOR FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                 81 GIGLILTGAYLD-------IKALDKNAPKAAFKWTWGKGMMLAGAVTM--- 121
                                                                                                                                                                                                                                                                        5 LIVVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKKDPIVPFLLNLFLGFGI---- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 DDSKSAFNLGAGEKLLAYETSKKDPIVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAV- 80
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: Patentin version 3.1 SEQ ID NO 51378 LENGTH: 479
                                                                                                                                                                                                                                   57; Indels 14;
                                                                                                                                                                                      Query Match 9.0%; Score 81; DB 6; Length 479; Best Local Similarity 27.6%; Pred. No. 4.7; Matches 35; Conservative 21; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.7%; Score 79; DB 6; Length 486; 28.9%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Mismatches
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; Sequence 78114, Application US/10282122A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 19571, Application US/10366683 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pseudomonas aeruginosa US-10-366-683-19571
                                                                                                                      ; ORGANISM: Bordetella pertussis US-10-282-122A-51378
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19571
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                                                                                                                                                                                                                                                                                                                                                                                                                                           GAVTMAV 123
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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8.7%; Score 78.5; DB 6; Length 372;
Best Local Similarity 21.7%; Pred. No. 6.1;
Matches 33; Conservative 30; Mismatches 46; Indels 4
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GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2001-12-27
PRIOR PELING DATE: 2001-12-27
PRIOR PELING DATE: 2001-12-27
PRIOR PELING DATE: 2001-12-27
PRIOR PELING DATE: 2001-12-29
PRIOR PELING DATE: 2001-12-29
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
                                                                                                                                                                                                          Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
Wall, Daniel
Trawick, John
Ohlsen, Kari
Zyskind, Judith
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; ORGANISM: Yersinia pestis
US-10-282-122A-78114
                                                                                                        Wall, Daniel
Trawick, John
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APPLICANT:
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TITLE OF INTERTION OF INTERTION OF ESSENTIAL Genes in Microorganisms FILE REPERRACE: ELITRA, 034A
CURRENT PLILIC DATE: 2003-02-20
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR PAPLICATION NUMBER: 60/200,848
PRIOR PAPLICATION NUMBER: 60/200,848
PRIOR PAPLICATION NUMBER: 60/200,321
PRIOR PAPLICATION NUMBER: 60/200,325
PRIOR PAPLICATION NUMBER: 60/200,335
PRIOR PAPLICATION NUMBER: 60/200,330
PRIOR PAPLICATION NUMBER: 60/200,330
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March 14, 2003, 20:13:37 ; Search time 29.3911 Seconds
  (without alignments)
  7815.311 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                       441362 seqs, 153338381 residues
                                                                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
                                                                                                                                                                                                           US-09-508-487-22
                                                                                                                                                                                                                                                                                          Scoring table:
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:* Issued_Patents_NA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	51 Sequence 651, App	Sequence 36, A	Sequence 288,	6 Sequence 36, 1	Sequence 11,	3 Sequence 13,	Sequence 1, 1	7	Sequence 2,		Sequence 11	Sequence 288, A	Sequence 32, A		27,	4, 4	~	4,	Sequence	Sequence 305	Sequence	Sequence 11,	Sequence 3, 1	472	24 Sequence 224,	Sequence 7, Ap	7,
SUMMARIES	ID	US-09-641-638-65	US-08-883-795A-36	US-08-998-416-288	US-08-883-795A-3	US-08-991-677-11	US-08-487-826B-1	US-08-446-855A-1	US-09-150-741-1	US-07-867-106-2	US-08-998-416-186	US-08-998-416-1137	US-08-998-416-288	US-08-617-860B-3	US-08-471-791-27	PCT-US91-01746-2	US-08-605-106-4	US-08-617-860B-33	US-08-605-106-4	US-08-451-405A-2	US-08-998-416-305	US-08-913-842-3	US-08-991-677-11	US-08-136-743B-3	US-08-998-416-47	US-08-998-416-22	US-08-713-000-7	US-08-975-316-7
	Query Match Length DB	20674 4	665 2	837 4	665 2	2251 4	19124 2	8920 2	8920 4	5852 1	615 4	636 4	837 4	1850 3	3440 1	3440 5	4098 2	1850 3	4098 2	731 1	834 4	2960 3	2251 4	2663 1		o.	1454 2	₹.
dР	Query		•		6.3	•	•	5.9		5.9	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7				5.5	5.5	5.5	5.4	5.4	5.4	5.4
	Score	51.4	49.6		47.2	46.8	45.2	44.4	44.4	44.2	42.8	42.8	42.8	42.8	42.8	42.8	42.8	42.6		42	42	41.4	41.2	41	40.6	40.4	40.4	40.4
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ALIGNMENTS

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LOCATION: 6429
OTHER INFORMATION: 10-347-165
NAME/KEY: allele
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LOCATION: 8703
OTHER INFORMATION: 10-349-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 6467
OTHER INFORMATION: 10-347-203
                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: 10-347-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 6611
OTHER INFORMATION: 10-347-348
NAME/KEY: allele
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OTHER INFORMATION: 10-348-391
NAME/KEY: allele
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LOCATION: 12429
OTHER INFORMATION: 10-350-332
                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 10-347-74
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                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
LOCATION: 6338
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
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LOCATION: 8658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : variable motif ATTTA or TTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : deletion of C
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                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: exon 14
MAME/RET: misc.feature
LOCATION: 17555. 20674
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COTHER INFORMATION: 10-508-245:
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284:
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295:
NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 10-513-352
NAME/KEY: allele
LOCATION: 2947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191
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OTHER INFORMATION: 10-343-231
NAME/KEY: allele
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NAME/KEY: allele
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LOCATION: 2341
OTHER INFORMATION: 10-512-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION: 10-511-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: 12-206-81
                                                                                                                                                                                                         ON: 13308..13429
INFORMATION: exon 11
                                                                                                                                                                                                                                                                                                                                            INFORMATION: exon 13
                                                                                                                                                                        INFORMATION: exon 10
                                                                                                                                                                                                                                                                                       INFORMATION: exon 12
                   NAME/KEY: exon
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
OTHER INFORMATION: exon 7
                                                                                                                 INFORMATION: exon 9
                                                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 16567..16667
                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 16775..16945
                                                                                               12254..12340
                                                                                                                                                    12854..13023
                                                                                                                                                                                                                                                                                                                                                                           17063..17554
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LOCATION: 2048
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LOCATION: 2323
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LOCATION: 2623
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LOCATION: 2934
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LOCATION: 2832
                                                                                                                                        NAME/KEY: exon
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                                                                                                 LOCATION:
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OTHER INFORMATION: 10-343-278 : polymorphic base C or T OTHER INFORMATION: 10-343-278 : polymorphic base C or T NAME/KEY: allele
COCATION: 4170
OTHER INFORMATION: 10-343-339 : polymorphic base G or T NAME/KEY: allele
COCATION: 5903
OTHER INFORMATION: 10-346-23 : polymorphic base A or G NAME/KEY: allele
COCATION: 6019
OTHER INFORMATION: 10-346-141 : polymorphic base A or G NAME/KEY: allele
COCATION: 6141
COCATION: 6141
COCATION: 6183
OTHER INFORMATION: 10-346-263 : polymorphic base G or C NAME/KEY: allele
COCATION: 6183
OTHER INFORMATION: 10-346-365 : polymorphic base C or T COCATION: 6183
OTHER INFORMATION: 12-206-366 : polymorphic base C or T
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JTHER INFORMATION: 10-507-170 : polymorphic base A or G

NAME/KEY: allele
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LOCATION: 12171
OTHER INFORMATION: 10-350-72 : polymorphic base C or T
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OTHER INFORMATION: 10-349-47 : polymorphic base C or T
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OTHER INFORMATION: 10-349-216: OTHER INFORMATION: 10-349-224: OTHER INFORMATION: 10-349-224: OTHER: INFORMATION: 10-349-368: OTHER INFORMATION: 10-349-368: OTHER INFORMATION: 10-349-368:
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OTHER INFORMATION: 10-347-220 :
NAME/KEY: 311ele
LOCATION: 6534
OTHER INFORMATION: 10-347-271 :
NAME/KEY: 311ele
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STATE:
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                                                                                                                                                                                                                                                                                                                                                 125 GTTCCAAAAGCCTTTTTTAAATTTCATTAATATGCTACCATAATACCAGTTTAATAAGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                        185 GGTTTTTATGAATAAGTTTTTAATTTTTTGGTAATCTTTTGTGCTTTTTCTAGTTT 244
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                                                                                                                                                                    Gaps
                                                                                                                                                                                                  5 ATTITCAACAAATAAAGATATIGTTAAAAGAATIGAAATIGCTAATTITATGGTTAAATC 64
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                                                                                                                             DB 4; Length 20674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application US/08883795A
Patent No. 5985607
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator NUMBER OF SEQUENCE: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 11413 AATTGCTTCAATATTAAATTTAAATTTTAATATTTTAATTTTAATATT 11459
                                                                                                                        6.9%; Score 51.4; DB 4; Length 2
48.7%; Pred. No. 0.0081;
tive 0; Mismatches 176; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 TGAAACTAATAAGAAAGATTCTCTTGTACCATTTTTATTGAACCTTT 351
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                                                     : polymorphic base C or
: polymorphic base A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERNIC/DOCKET NUMBER: 7841-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/883,795A FILING DATE: 27-JUN-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
               NAME/KEY: allele
LOCATION: 13524
OTHER INFORMATION: 10-507-353
OTHER INFORMATION: 10-507-321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                              Matches 169; Conservative
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COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore
                                                                                                                                               Similarity
                                                                      NAME/KEY: allele
LOCATION: 13535
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                                                                                                                            Query Match
                                                                                                                                                Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 GTTTATAATTACATATTTTATAATTACATATTTTATAAAGTATTTATAATTACATATTT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTCCAAAAGCCTTTTTAAATTTCATTAATATGCTACCATAATACCAGTTTAATAAAGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 СТТТАТААТТАСАТАТТТАТААТТААААТСТТТАТААТТАСАТАТТТАТААТТААААТ 366
                                                                                                                                                                                                                                                                                                                                                                                                   65 AAGAAGCTCTATTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAAGTTAAAATA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 TGCTCAAGATGATTCTAAAAGCACTTTTAATCTGGGAGCGGGAGAAAATTTTTGGTTTA 304
                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                        5 ATTITCAACAAATAAAGATAITGITAAAAGAAITGAAATTGCTAATTITATGGTTAAATC
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                                                                                                                                                                                                                Length 665;
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                                                                                                                                                                                                         Score 49.6; DB 2; Pred. No. 0.0094; O; Mismatches 189;
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APPLICANT: Pohilippsen, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Wohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUEN
TITLE OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 288, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
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No. 6239264th Carolina
Y: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                              6.6%;
llarity 46.3%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                         ; IMMEDIATE SOURCE:
; CLONE: Rh 32
US-08-883-795A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
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CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 62392
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MEDIUM TYPE: Floppy
                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
STRANDEDNESS: Sil
TOPOLOGY: linear
                                                                                                                                                                                                                                    Best Local Similarity
Matches 163; Conserv
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us-09-508-487-22.rni

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Gravelle, Micheline AATION NUMBER: 40,261
                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pinus taeda
                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                             MOLECULE TYPE: O
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US-08-883-795A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491 TAAGAAATTAAAGTTAAAATTAATTTTAATAATAATTCTTATAAAAGATTAAATAATAT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 GTTTTARGAATAAGTTTTTAATTTTAGTAATCTTTTGTGCTTTTTCTAGTTTT 245
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Vectors for Tissue Plasminogen Activator
                                                                                                                                                                                                                                                                                                                        Score 48.6; DB 4; Length 837;
Pred. No. 0.017;
0; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ralease #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                        PF/5-30306/A/CGC1976
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FILING DATE: 27-JUN-1997
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Patent No. 5985607
GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
ITLE OF INVENTION: Recombinant DNA
TITLE OF INVENTION: Vectors for Tiss
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSE:
ADDRESSEE: BERESKIN & PARR
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-
TELECOMMUNICATION INFORMATION:
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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40 King Street West
                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                        Query Match 6.5%;
Best Local Similarity 46.6%;
Matches 156; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                PAG1241RP
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                                                                                                                                                                                                                                              ORIGINAL SOURCE:
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US-08-998-416-288
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61 AATCAAGAAGCTCTAUTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAGTTAAATTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AATAGTTCCAAAAGCCTTTTTTAAATTTCATTAATATGCTACCATAATACCAGTTTAATA 180
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APPLICANT: Carraway, Daniel T
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REPERBORCE: 50617
CURRENT APPLICATION NUMBER: US/08/991,677A
CURRENT FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: US 60/033,381
EARLIER FILING DATE: 1996-12-16
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47.2; DB 2; Length 6 Pred. No. 0.032; 0; Mismatches 193; Indels
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REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-
TELEPHONE: (416) 364-7311
TELEPHONE: (416) 361-1398
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.3%;
Best Local Similarity 45.8%;
Matches 163; Conservative
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Matches 102; Conservative
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154 ATATGCTACCATAATACCAGTTTAATAAAGGGGTTTTTATGAATAAGTTTTTAATTTTTA 213
                                                                                                                                                     334 CATTTTTATTGAACCTTTTTTAGGGTTCGGGATAGGTTCTTTTGCTCAAGGAGATATCC 393
                                                                                                                                                                                                                                                                                                         394 TIGGAGGITCICITATICITGGAITIGATGCGGTTGGTATAGGGTTAATACTTACAGGAG
                                                                          TTTTGGTAATCTTTTGTGCTTTTTTTTTTTTTTGCTCAAGATGATTCTAAAAGCACTTTTA
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APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   454 CITAITIGGACATCAAGGATTITGATAATAATGCTAAAAAAGCTGATTTT 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/446,855A FILING DATE: 06-Jul-1995 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION
TELEPHONE: 703-816-4000
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.8
Matches 135; Conservative
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MEDIUM TYPE: Floppy
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: USA
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APPLICANT: Chitnis, Chetan
APPLICANT: Miler, Louis H.
APPLICANT: Miler, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ENTTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
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                                                                          CGAATTTCGAGTAACAATTTGAAAAAGTTAAATTTTAAATAGTTCCAAAAGCCTTTTTTA 143
                                                                                                  144 AATTTCATTAATATGCTACCATAATACCAGTTTAATAAAGGGGTTTTTATGAATAAGTTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 GTAACAATTTGAAAAAAGTTAAATTTTAAATAGTTCCAAAAGCCTTTTTTAAATTTCATTA 153
24 ATTGTTAAAAGAATTGAAATTGCTAATTTTATGGTTAAATCAAGAAGCTCTATTGGTAAG 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B FILING DATE: 10-SEP-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45.2; DB 2;
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-6176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                          US-08-487-826B-13/c; Sequence 13, Application US/08487826B patent No. 5993827; Betni INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                   799 TGTTGGTAAATTT 812
                                                                                                                                                                                                                            204 TTAATTTTATTT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 182; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                  19103
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US-07-867-106-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                     COUNTRY:
   US-07-867-106-2
                                                                                                                                                                                                                      STATE:
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TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 618396
TITLE OF INVENTION: Synthetase II
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: P633/00617
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
                                                                              61 AATCAAGAAGCTCTATTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAAGTTAAATTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AATCAAGAAGCTCTATTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAAGTTAAATTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AATAGTICCAAAAGCCTTTTT----TAAATTTCATTAATATGCTACCATAATACCAGTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 TAATAAAGGGGTTTTTATGAATAAGTTTTTAATTTTTAGTAATCTTTTGTGCTTT 235
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1 TAGAATTITCAACAAATAAAGATATTGTTAAAAGAATTGAAATTGCTAATTTTATGGTTA
                                                                                                                        121 AATAGTTCCAAAAGCCTTTTT----TAAATTTCATTAATATGCTACCATAATACCAGTT
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Best Local Similarity 50.8%; Pred. No. 0.24;
Matches 135; Conservative 0; Mismatches 126;
                                                                                                                                                                                                                                                                           8493 ATATATTATACTTTTCATGTTGTTA 8468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-150-741-1
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2201 ТІТСАТТААТТІТІТІТІТІТІТІТІТІТІТТТАААЛІТІСТІТІТІТІТІТІТІТІТІТІТТТТТ 2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 CTCTATTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAGTTAAATTTAAATAGTTCCA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                        APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
NUMBER OF EXQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 AAAGCCTTTTTTAAATTTCATTAATATGCTACCATAATACCAGTTTAATAAGGGGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5852;
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Pred. No. 0.25;
0; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
Sequence 2, Application US/07867106
Patent No. 3389526
GENERAL INFORMATION:
APPLICANT: Slade, Martin B
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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NUCLEIC ACID
EDNESS: single
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2378..5038
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Best Local Similarity
Matches 118; Conserva
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239 TAGTTTTGCTCAAGATGATTCTAAAAGCACTTTTAATCTGGGAGCGGGAAAAATTTTT 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wohr, Christine
APPLICANT: Wohr, Christine
APPLICANT: Mendland, Jurgen
APPLICANT: Reachile, Jurgen
APPLICANT: Rechile, Dinipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: No. 622267
STRPPP
                                                                                                                                                                                                                                          299 GGTTTATGAAACTAATAAGAAAGATTCTCTTGTACCATTTTTATTGAACCTTTTTT 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENTON OF CLASSIPTAMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cormualls Road CITY: Research Triangle Park STATE: No. 6239264th Carolina
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-303
TELEPHONE: 919-541-8689
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1137, Application US/08998416 Patent No. 6239264
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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US-08-998-416-1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 TAAATAGTTCCAAAAGCCTTTTTTAAATTTCATTAATATGCTACCATAATACCAGTTAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 TCATCATTATTAATATTATAATTATAAAAATAATTATTAATATGAATACTATTTAGT 218
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APPLICANT: Steiner, Sabine
APPLICANT: Whit, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
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Pred. No. 0.3;
0; Mismatches 187; Indels
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
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FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTOMACE MAGENT INFORMATION:
NAME: Medigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                   Sequence 186, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
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TELECOMMUNICATION INFORMATION:
TELEFONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
ORGANISM: PAG1074RP
                                                                                                                                                                                                                                                                                                         Philippsen, Peter
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 46.9°
Matches 167; Conservative
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APPLICANT: Philip
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179 TAAAGGGGTTTTTATGAATAAGTTTTTAATTTTTATTTTGGTAATCTTTTGTGCTTTTTC 238
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                                                          TAAATAGTTCCAAAAGCCTTTTTTAAATTTCATTAATATGCTACCATAATACCAGTTTAA 178
                                                                                                                                                                                                                                                    279 AAATTATTAAATAGATTATCAATAATTAATATTATTATTAATTGTTTATTAAATAA 338
                                                                                                                                                           299 GGTTTATGAAACTAATAAGAAAGATTCTCTTGTACCATTTTTATTGAACCTTTTTT 354
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Wohr, Christine
APPLICANT: Wordland, Jurgen
APPLICANT: Receiver, Philipp
APPLICANT: Receiver, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 288, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
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APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PE,
TELECOMMUNICATION:
TELEPHONE: 919-541-8887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Philippsen, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 837 base pairs
nucleic acid
EDNESS: single
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US-08-998-416-288
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DB 4; Length 837;

5.7%; Score 42.8;

Query Match

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                                                                                                                                                                                                                                                                                                                                                    179 TAAAGGGGTTTTTATGAATAAGTTTTTAATTTTTATTTTGGTAATCTTTTGTGCTTTTTC 238
                                                                                                                                                                                                                                                                                                                                                                                                239 TAGTTTTGCTCAAGATGATTCTAAAAGCACTTTTAATCTGGGAGGGGGAGAAAATTTTT 298
                                                                                                                                                             61 AATCAAGAAGCTCTATTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAAGTTA--AATT 118
                             Gaps
                                                                   TAGAATTTTCAACAAATAAAGATATTGTTAAAAGAATTGAAATTGCTAATTTTATGGTTA 60
                                                                                                                 39 TAAACTTTTTTATTATAATATTTAAGTATTAAAATTATTTAAACTATTATTATCATTATTT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 GGTTTATGAAACTAATAAGAAAGATTCTCTTGTACCATTTTTATTGAACCTTTTTT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Typfer, R., Bautor, J., Bothmann, H., Filsak, E., APPLICANT: Hvricke-Grandplerre, C., Klein, B., Martini, N., APPLICANT: Miler, A., Schulte, W., Voetz, M., Walek, J., APPLICANT: Schell, J.
                     0; Mismatches 187; Indels
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APPLICATION NUMBER: US/08/617,860B
FILING DATE: 01-MAR.1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steinberg, Raskin & Davidson, P.C
  46.9%; Pred. No. 0.32;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02950
FILING DATE: 05-SEP-1994
APPLICATION NUMBER: DE P4329951.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: DE P4329951.2 FILING DATE: 04-SEP-1993 INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32, Application US/08617860B Patent No. 6133506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...ridCanT: Schell, J.
TITLE OF INVENTION: Promoters
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steiner
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CLONE: ClTEg1
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IMMEDIATE SOURCE:
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Nucleic acid
                     167; Conservative
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Best Local Similarity
Matches 167; Conserv
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ORIGINAL SOURCE:
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2345 GTTTCAAAAAATTTCAAAAAAAAAAATTTCAAAAAAGAAAATTTAAAAAAGGGAATTTAA 2286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AATCAAGAAGCTCTATTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAAGTTAAATTTA 120
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Sequence 27, Application PC/TUS9101746
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Knauf, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.7%; Score 42.8; DB 1; Length 3 52.1%; Pred. No. 0.45; tive 0; Mismatches 107; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
                                                                                                                                                                                                                                                                                                                                                                           CGNE 69-5
          CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
PRIOR APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
PRIOR APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MARTION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: DONNA E. SCHORET
REGISTRATION NUMBER: 31,845
NAME: DONNA E. SCHORET
REGISTRATION NUMBER: 31,845
                                                                                                                                                                                                                                                                                                                                                                   REFERENCE DOCKET NUMBER: CGNI TELECOMMUNICATION INFORMATION: TELEPHONE: (916) 753-613 TELEX: 350370 CGNE INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS: LENGTH: 3440 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MicrosoftWord 4.0
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STREET: 1920 Fifth Street
CITY: Davis
STATE: California
14-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                            NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 1850;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 42.8; DB 3; Length 1:
Pred. No. 0.39;
0; Mismatches 119; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Thompson, Gregory A
APPLICANT: Knauf, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01746
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APPLICATION NUMBER: 07/762,762
FILING DATE: 16-SEPT-1991
CLASSIFICATION: 435
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Patent No. 5723595
                                                                                                                                           Transcription start
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1797..1850
                 CAAT-Signal
1428..1432
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1553..1556
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1642..1657
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1797..1799
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California
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Best Local Similarity
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US-08-471-791-27/C
                                                                           NAME/KEY:
LOCATION:
FEATURE:
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US-08-617-860B-32
               NAME/KEY:
LOCATION:
                                                                                                                                         NAME/KEY:
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NAME/KEY:
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                                         FILING DATE: LUSICAL
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR: 1990
APPLICATION NUMBER: 31,845
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: 34,719
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: ATA:8;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01746
FILING DATE: 19910314
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Job time : 58.3911 secs
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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 14:24:31; Search time 145.333 Seconds

(without alignments)
789.650 Million cell updates/sec
904
Sequence: 904
Sequence: 1 MNKFLIVVLLAFCVFSSFAQ.......DINMGQASALGFELSFKKSY 178
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 4569144 seqs, 644733110 residues
Total number of hits satisfying chosen parameters: 4569144
Minimum DB seq length: 2000000000
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query

No. Score Match Length DB ID

1 904 100.0 178 15 US-09-153-447-21 Sequence 21, Ap 2 904 100.0 178 15 US-09-156-447-21 Sequence 21, Ap 3 904 100.0 178 19 US-09-508-487-21 Sequence 21, Ap 4 786.5 87.0 177 15 US-09-156-447-23 Sequence 23, Ap 5 786.5 87.0 177 15 US-09-156-447-23 Sequence 23, Ap 6 786.5 87.0 177 19 US-09-508-487-23 Sequence 23, Ap 6 786.5 87.0 177 19 US-09-508-487-23 Sequence 23, Ap

Sequence	Sednence 19,	Sequence 19,	Sequence 31,	Sequence 31	Sequence 31	22 Sequence 91	Sequence 1,	Segmence 1	Secuence 1	'T application of	sednence 24	8 Sequence 40	0 Seguence 68	69 Sequence 13	69 Sequence 13169,	0 Sequence 53	7 Sequence 5927,	81 Sequence	Sequence 896,	82 Sequence 5882	13 Sequence	13 Sequence 2041	5 Sequence 9355, A	72 Sequence	41 Sequence 13341	4 Sequence	Sequence 95,	41 Sequence 1334	41 Sequence 1334	0 Sequence 2950	72 Seguence 4607	.71 Sequence 3217	.6 Sequence 1216,	Seguence 482,	Sequence 482,	27 Sequence 6827,	Sequence 22, A	Sequence 22, A	Sequence	•			
15 US-09-153-447-19	15 US-U9-156-447-19	19 US-09-508-487-19	15 US-09-153-447-31	15 US-09-156-447-31	19 US-09-508-487-31	21 US-09-791-537-919	US-09-153-447-1	15 US-09-156-447-1	19 175-00-508-487-1	1 /0+ 000 CO CO	20 US-U9-6U2-/B/A-54	US-09-603-024C-4	US-09-738-626-68	US-09-739-449-13	US-09-803-110-13	US-09-134-000-53	US-09-328-352-59	US-08-993-002A-5	US-08-625-811-89	13 US-08-993-002A-58	US-09-248-796-20	US-60-096-409-20	US-10-179-131	ns-60-360-03	PCT-US02-03987-13	US-09-583-11(us-09-769-787	US-09-815-242	US-10-072-851-	US-09-107-43	US-10-219-999-	US-60-324-109-	PCT-US98-06371-	US-08-902-615A	US-09-882-227-	US-09-488-725A	US-09-611-419A	US-09-910-186A-2	US-60-360-039-48		!	ALIGNMENTS	
85.1 179	1.0	5.1	7.7	7.7	7.7	7.7	3.7	3.7	7 7			0.7	0.7	.7 6	.7	.6	.5	.5	.5	.5	.3	.3	.3 16	.2	.2	.2	.2	.2	.2	.2	.2	.2	.1	.1	.1	.0	.0	.0	9 0.				
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	S3447 NS FROM BORRELIA (09/153,447 5 (059,036 41/97 Score 904; DB 15; Length 178; Pred. No. 1.8e-92; Indels 0; Prismatches 0; SKSAFNLGAGEKLLAYETSKKDPIVPELINLELGEC	pplication US/09153447 ATION: ATION: ATION: SATION: SATION: SVEN NUTION: P13 ANTIGENS FROM BORRELIA E: 454312-3130.1 CATION NUMBER: US/09/153,447 CATION NUMBER: 60/059,036 G DATE: 1997-09-10 G DATE: 1997-09-10 ID NOS: 31 entIn Ver. 2.1 ITERIA afzelii INCO.0%: Score 904; DB 15; Length 178; Illarity 100.0%: Pred. No. 1.8e-92; CONSERVATIVE 0; Mismatches 0; Indels 0;	pplication US/09153447 ATION: RGSTROM, Sven NTTON: P13 ANTIGENS FROM BORRELIA E: 454312-3130.1 CATION NUMBER: US/09/153,447 G DATE: 1998-09-15 G DATE: 1997-09-10 CATION NUMBER: 1041/97 G DATE: 1997-09-10 CATION NUMBER: 1041/97 G DATE: 1997-09-10 TD NOS: 31 entin Ver. 2.1 100.0%; Score 904; DB 15;	Sequence 21, Application US/09153447 Sequence 21, Application US/09153447 GENERAL INFORMATION: APPLICART: BERGSTROW, Sven TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA FILE REFERENCE: 454312-3130.1 CURRENT APPLICATION NUMBER: US/09/153,447 CURRENT FILING DATE: 1998-09-15 EARLIER APPLICATION NUMBER: 06/059,036 EARLIER APPLICATION NUMBER: 1041/97 EARLIER PILING DATE: 1997-09-10 SARLIER FILING DATE: 1997-09-10 SARLIER PILING DATE: 1997-09-10 SARLIER PILING DATE: 1207-09-10 SARLIER PILING DATE: 1207-09-10 SARLIER PILING DATE: 137-09-10 SOFTWARE: PATHING DATE: 137-09-10	Sequence 21, Application US/09153447 Sequence 21, Application US/09153447 GENERAL INFORMATION: PAPLICANT: BERGSTROM, Sven TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA CURRENT APPLICATION NUMBER: US/09/153,447 CURRENT FILING DATE: 1998-09-15 EARLIER APPLICATION NUMBER: 60/059,036 EARLIER FILING DATE: 1997-09-10 EARLIER FILING DATE: 1997-09-10 NUMBER OF SEQ ID NOS: 31 SOFTWARE: PATENTION OF SEQ ID NOS: 31 SEQ ID NO 21 LENGTH: 178 TYPE: PRT	Sequence 21, Application US/09153447 GENERAL INFORMATION: APPLICANT: BERGSTROW, Sven TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA FILE REPERBUES: 454312-3130.1 CURRENT APPLICATION UNDABER: 0S/09/153,447 CURRENT FILING DATE: 1998-09-15 EARLIER APPLICATION NUMBER: 60/059,036 EARLIER FILING DATE: 1997-09-10 EARLIER FILING DATE: 1997-09-10 SEARLIER FILING DATE: 1997-09-10 SEARLIER FILING DATE: 1997-09-10 SERVIDE PAPPLICATION NUMBER: 1041/97 SARVIDE NOS: 31 SSOID NOS: 31 SSOID NOS: 31	Sequence 21, Application US/09153447 GENERAL INFORMATION: APPLICANT: BERGSTROM, Sven TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA CURRENT APPLICATION UNBER: US/09/153,447 CURRENT FILING DATE: 1998-09-15 EARLIER APPLICATION UNBER: 60/059,036 EARLIER FILING DATE: 1997-09-10 EARLIER FILING DATE: 1997-09-10 SEARLIER FILING DATE: 1997-09-10 SEARLIER FILING DATE: 1997-09-10 SEARLIER FILING DATE: 1997-09-10 SEARLIER FILING NOTE: 2.1	Sequence 21, Application US/09153447 GENERAL INFORMATION: APPLICANT: BERGSTROM, Sven TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA CURRENT APPLICATION NUMBER: US/09/153,447 CURRENT FILING DATE: 1998-09-15 EARLIER RAPLICATION NUMBER: 60/059,036 EARLIER FILING DATE: 1997-09-10 EARLIER FILING DATE: 1997-09-10 EARLIER FILING DATE: 1997-09-10 MUMBER OF SEO ID NOS: 31	Sequence 21, Application US/09153447 GENERAL INFORMATION: APPLICANT: BERGSTROM. Sven TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA FILE REFERENCE: 454312-3130.1 CURRENT APPLICATION NUMBER: US/09/153,447 CURRENT FILING DATE: 1998-09-15 EARLIER FILING DATE: 1997-09-10 EARLIER FILING DATE: 1997-09-10 EARLIER FILING DATE: 1997-09-10 EARLIER FILING DATE: 1997-09-10	Sequence 21, Application US/09153447 GENERAL INFORMATION: APPLICANT: BERGSTROM, Sven TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA FILE REFERENCE: 454312-3130.1 CURRENT REPERIOR: US/09/153,447 CURRENT FILING DATE: 1998-09-15 EARLIER APPLICATION NUMBER: 60/059,036 EARLIER APPLICATION NUMBER: 60/059,036 EARLIER APPLICATION NUMBER: 1041/97	Sequence 21, Application US/09153447 GENERAL INFORMATION: APPLICANT: BERGSTROM, Sven TITLE OF INVENTION: P13 ANTICENS FROM BORRELIA FILE REFERENCE: 454312-3130.1 CURRENT APPLICATION NUMBER: US/09/153,447 EARLIER APPLICATION NUMBER: 60/059,036 EARLIER PILING DATE: 1997-09-10	<pre>; Sequence 21, Application US/09153447 ; GENERAL INFORMATION: APPLICANT: BERGSTROM, Sven ; TITLE OF INVENTION: P13 ANTICENS FROM BORRELIA ; FILE REFERENCE: 454312-3130.1 ; CURRENT APPLICATION NUMBER: US/09/153,447 ; CURRENT FILING DATE: 1998-09-15 ; EARLIER APPLICATION NUMBER: 60/059,036</pre>	; Sequence 21, Application US/09153447 ; GENERAL INFORMATION: A APPLICANT: BERGSTROW, Sven ; TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA ; FILE REFERENCE: 454312-3130.1 ; CURRENT APPLICATION NUMBER: US/09/153,447 ; CURRENT FILING DATE: 1998-09-15	; Sequence 21, Application US/09153447 ; GENERAL INFORMATION: A APPLICANT: BERGSTROM, Sven TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA ; FILE REPERENCE: 454312-3130.1 ; CURRENT APPLICATION NUMBER: US/09/153,447	<pre>; Sequence 21, Application US/09153447 ; GENERAL INFORMATION: ; APPLICANT: BERGSTROM, Sven ; TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA : FITE REFERENCE: 454312-3130.1</pre>	; Sequence 21, Application US/09153447 ; GENERAL INFORMATION: ; APPLICATE: BESESTROM; Sven	; Sequence 21, Application US/09153447 ; GENERAL INFORMATION:	; Sequence 21, Application US/09153447		

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RESULT 5
US-09-156-447-23
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Matches 154;
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                GSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAVT 120
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                                                                MAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASALGFELSFKKSY 178
                                                                               MAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASALGFELSFKKSY 178
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100.0%; Pred. No. 1.8e-92;
tive 0; Mismatches 0;
                                                                                                                                                                                                       APPLICANT: BERGSTROM, SVen
TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA
FILE REFERENCE: 454312-3130.1
CURRENT APPLICATION NUMBER: U5/09/156,447
CURRENT FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 06/059,036
PRIOR APPLICATION NUMBER: 1041/97
PRIOR APPLICATION NUMBER: 1041/97
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver: 2.1
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GENERAL INFORMATION:
APPLICANT: BERGETROM, Sven
TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA
FILE REFERENCE: 454312-3150
CURRENT APPLICATION NUMBER: US/09/508,487
CURRENT FILING DATE: 2000-03-10
PRIOR PELICATION NUMBER: 60/059,036
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1998-09-04
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; Sequence 21, Application US/09156447
; GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Borrelia afzelii
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Best Local Similarity 100.
Matches 178; Conservative
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US-09-508-487-21
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Matches 178; Conserv
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                           1 MNKFLIVVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKKDPIVPFLLIVFLGFGI 60
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Pred. No. 2.6e-79;
7; Mismatches 16;
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CURRENT APPLICATION NUMBER: US/09/156,447
CURRENT FILING DATE: 1998-09-15
FRIOR APPLICATION NUMBER: 60/059,036
PRIOR FILING DATE: 1997-09-10
PRIOR PILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 23
LENGTH: 177
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TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA
FILE REFERENCE: 454312-3130.1
CURRENT APPLICATION NUMBER: US/09/153,447
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION NUMBER: 60/059,036
EARLIER APPLICATION NUMBER: 1041/97
EARLIER APPLICATION NUMBER: 1041/97
EARLIER APPLICATION NUMBER: 1041/97
SARLIER FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                     ; Sequence 23, Application US/09153447; GENERAL INFORMATION:
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illarity 86.5%;
Conservative
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US-09-156-447-23
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                                          Gaps
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    DB 15; Length 177;
                                          Indels
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GENERAL INFORMATION:
APPLICANT: BERGSTROM, Sven
: TITLE OF INVENTION: PANTIGENS FROM BORRELIA
: FILE REFERENCE: 454312-3150
: CURRENT APPLICATION NUMBER: US/09/508,487
: CURRENT PAPLICATION NUMBER: 06/059,036
: PRIOR FILING DATE: 1997-09-10
: PRIOR PILING DATE: 1997-09-10
: PRIOR FILING DATE: 1997-09-10
: PRIOR FILING DATE: 1998-09-04
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PATENTIN VET. 2.1
: SOFTWARE: PATENTIN VET. 2.1
Score 786.5; DB 15;
Pred. No. 2.6e-79;
7; Mismatches 16;
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Pred. No. 2.6e-79;
7; Mismatches 16;
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TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA
FILE REFERENCE: 454312-3130.1
FURRENT APPLICATION NUMBER: US/09/153,447
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION NUMBER: 60/059,036
EARLIER FILING DATE: 1997-09-10
EARLIER FILING DATE: 1997-09-10
EARLIER FILING DATE: 1997-09-10
SARVIER FILING DATE: 1997-09-10
SOFTWARE: PATENTING NOWER: 1041/97
SOFTWARE: PATENTING NOWER: 1057-09-10
SOFTWARE: PATENTIN VET: 2.1
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87.0%;
86.5%;
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86.5%;
                      Best Local Similarity 86.5 Matches 154; Conservative
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US-09-508-487-23
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Matches 154; Conservative
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US-09-508-487-23
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                                                                                                                                              Gaps
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                                                                                                   Length 179;
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                                                                                                     DB 15;
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                                                                                                   85.1%; Score 769.5; DB 15;
84.9%; Pred. No. 2.1e-77;
ive 10; Mismatches 16;
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CURRENT APPLICATION NUMBER: US/09/508,487
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/059,036
PRIOR APPLICATION NUMBER: 197-09-10
PRIOR APPLICATION NUMBER: 1041/97
PRIOR FILING DATE: 1997-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P13 ANTIGENS FROM BORRELIA
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TITLE OF INVENTION: P13 ANTIGENS FROM BORRE
FILE REFERENCE: 454312-3130.1
CURRENT APPLICATION NUMBER: US/09/156,447
CURRENT FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/059,036
PRIOR APPLICATION NUMBER: 1041/97
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 19, Application US/09156447; GENERAL INFORMATION:
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; APPLICANT: BERGSTROM, Sven
LENGTH: 179
TYPE: PRT
ORGANISM: Borrelia burgdorferi
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ORGANISM: Borrelia burgdorferi
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Best Local Similarity 84.9%
Matches 152; Conservative
                                                                                                                       Best Local Similarity 84.9
Matches 152; Conservative
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PRIOR FILING DATE:
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US-09-791-537-91922
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                                                          SEQ ID NO 31
LENGTH: 95
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LENGTH: 95
                                                                                                  TYPE: PRT
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17.7%; Score 160; DB 15;
Best Local Similarity 44.4%; Pred. No. 2.1e-09;
Matches 36; Conservative 12; Mismatches 31;
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CURRENT APPLICATION NUMBER: US/09/153,447

CURRENT FILING DATE: 1998-09-15

EARLIER APPLICATION NUMBER: 60/059,036

EARLIER FILING DATE: 1997-09-10

EARLIER FILING DATE: 1997-09-10

EARLIER FILING DATE: 1997-09-10

EARLIER FILING DATE: 1997-09-10

WHIGHER OF SEQ ID NOS: 31
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TITLE OF INVENTION: P13 ANTICENS FROM BORRELIA
FILE REFERENCE: 454312-3130.1
CURRENT APPLICATION NUMBER: US/09/156,447
CURRENT FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/059,036
PRIOR FILING DATE: 1997-09-10
PRIOR APPLICATION NUMBER: 1041/97
PRIOR APPLICATION NUMBER: PCT/IB98/01424
PRIOR FILING DATE: 1998-09-04
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GENERAL INFORMATION:
APPLICANT: BERGSTROM, Sven
                                                                                                                                   ; ORGANISM: Borrelia burgdorferi
US-09-508-487-19
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                                                        PatentIn Ver. 2.1
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SEQ ID NO 31
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                                  NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ver
SEQ ID NO 19
LENGTH: 179
TYPE: PRT
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US-09-153-447-31
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APPLICANT: Bionomit, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Deseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME.
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: 2001/02-22
CURRENT FILING DATE: 2001-02-22
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: P13 ANTIGENS FROM BORRELIA
FILE REPERENCE: 454312-3150
CURRENT APPLICATION WURBER: U5/09/508,487
CURRENT FILING DATE: 2000-03-10
PRIOR PILING DATE: 1997-09-10
PRIOR PILING DATE: 1997-09-10
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VOYE: 2.1
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Best Local Similarity 44.4%; Pred. No. 2.1e-09;
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44.4%; Pred. No. 2.1e-09;
iive 12; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 GSFVQGDYIGGGSVLGFNLLG 79
                                                                                                                                           ; ORGANISM: Borrelia burgdorferi
US-09-156-447-31
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US-09-508-487-31
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1997-09-10
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                    NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver.
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Best Local Similarity
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                                                                                                              Query Match 17.7%; Score 160; DB 21; Length 95; Best Local Similarity 44.4%; Pred. No. 2.1e-09; Matches 36; Conservative 12; Mismatches 31; Indels
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96.0%; Pred. No. 4.3e-06;
tive 1; Mismatches 0;
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US-09-156-447-1

Sequence 1, Application US/09156447

SEQUENCE 1, Application US/09156447

SEQUENCE 1, BERGSTROM, SVEN

TILLE OF INVENTION: P13 ANTIGENS FROM BORRELIA

FILE REFERENCE: 454312-3130.1

CURRENT APPLICATION NUMBER: US/09/156,447

CURRENT FILING DATE: 1998-09-15

PRIOR FILING DATE: 1997-09-10

PRIOR FILING DATE: 1997-09-10

NUMBER OF SEQ ID NOS: 31

SEQUENCE: Patentin Ver. 2.1

SEQUENCE: ALLONG PATENTING DATE: US/09-10

NUMBER OF SEQ ID NOS: 31

SEQUENCE: Patentin Ver. 2.1
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GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 454312-3130.1

CURRENT APPLICATION NUMBER: US/09/153,447

CURRENT FILING DATE: 1996-09-15

EARLIER FILING DATE: 1996-09-16

EARLIER FILING DATE: 1997-09-10

EARLIER PELING DATE: 1997-09-10

SAFRIER PELING DATE: 1997-09-10

SOFTWARE: PAPLICATION VUMBER: 1041/97

EARLIER FILING DATE: 1997-09-10

SOFTWARE: PAPLICATION VERE: 1977-09-10

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                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Borrelia burgdorferi
US-09-156-447-1
                                             ; ORGANISM: Borrelia burgdorferi
US-09-791-537-91922
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Best Local Similarity 96.0°
Matches 24; Conservative
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US-09-153-447-1
LENGTH: 95
TYPE: PRT
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Search completed: March 14, 2003, 14:35:07 Job time: 146.333 secs

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OM protein - protein search, using sw model

March 14, 2003, 14:25:51; Search time 10 Seconds Run on:

(without alignments) 820.439 Million cell updates/sec

US-09-508-487-21 904 Perfect score: Title:

1 MNKFLIVVLLAFCVFSSFAQ......DINMGQASALGFELSFKKSY 178 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

199416 segs, 46092074 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Dogoriation	Describcion	Sequence 6850, Ap	Sequence 13341, A	Sequence 22, Appl	Sequence 25, Appl	Sequence 10070, A	Sequence 14080, A	Sequence 5875, Ap	Sequence 13058, A	Sequence 11462, A	Sequence 20, Appl	Sequence 422, App	Sequence 16, Appl	Sequence 16, Appl	Sequence 4426, Ap	Sequence 134, App	Sequence 19, Appl	φ	~	Sequence 10662, A
	£	at a	US-09-738-626-6850	US-09-815-242-13341	US-09-910-186A-22	US-10-011-588-25	US-09-815-242-10070	US-09-815-242-14080	US-09-815-242-5875	US-09-815-242-13058	US-09-815-242-11462		US-09-741-669-422	US-09-925-637-16	US-09-881-752A-16	US-09-738-626-4426	US-09-860-670-134	US-09-886-468-19	US-09-215-450-26	US-09-815-242-4932	US-09-815-242-10662
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dР	Query		10.7	9.5	9.0	9.0	8.7	8.7	8.4	8.4	8.4	8.1	8.0	8.0	7.9	7.9	7.9	7.9	7.9	7.8	7.8
	aros	3000	97	83.5	81.5	81.5	78.5	78.5	97	16	75.5	73.5	72.5	72	71.5	71.5	71.5	71.5	71	70.5	70.5
	Result		1	7	e	4	S	9	7	89	6	10	11	12	13	14	15	16	17	18	19

Sequence 5123, Ap Sequence 11246, A Sequence 6860, Ap Sequence 6811, Ap Sequence 5631, Ap Sequence 12384, A Sequence 2, Appl Sequence 11312, A Sequence 11212, A Sequence 11212, A Sequence 5281, Ap Sequence 5281, Ap Sequence 5281, Ap Sequence 5281, Ap Sequence 5281, Ap Sequence 5281, Ap Sequence 5381, Ap Sequence 5384, App Sequen	Sequence 1230 Sequence 6, Ap. Sequence 11817, A Sequence 3927, Ap. Sequence 2, Appli Sequence 11858, A Sequence 6, Appli
US-09-738-626-5123 US-09-738-626-4875 US-09-738-626-6860 US-09-738-626-6860 US-09-738-626-6861 US-09-738-626-6861 US-10-217-096-4 US-09-815-242-1384 US-09-912-183A-2 US-09-912-183A-2 US-09-912-1384 US-09-912-11380 US-09-915-242-11380 US-09-815-242-11384 US-09-815-242-11384 US-09-815-242-11380 US-09-815-242-11212 US-09-815-242-11212 US-09-815-242-11212 US-09-815-242-11212 US-09-815-242-11212 US-09-815-242-11212	D D
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669 699 699 699 699 699 604 607 607 607 607	66 66 66 66 66 66 66
010000000000000000000000000000000000000	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

48 VP-FLLNLFLGFGIGSFAQGDIL-----GGFLILGFDAVGIGLILTGAYLDIKALDKNA 100 80; Gaps Query Match 10.7%; Score 97; DB 9; Length 417; Best Local Similarity 23.1%; Pred. No. 0.022; Matches 50; Conservative 24; Mismatches 62; Indels 5 LIVVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKK-TYPE: PRT; ORGANISM: Corynebacterium glutamicum US-09-738-626-6850 US-09-738-626-6850 q ò ò

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ORGANISM: Artificial Sequence
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101 PKAAFKWTWGKGMMLAGAVTWAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEP---- 156
                                                                                                        233 PWKLFK-----NMLPAYFTALGISSSAATIPVI----YQQTLKNDVDVNVAGFVVPLCA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 AGALVLAIKKYVKVPRSLEGAKSILLLPLLGTILTGFVMLAVNIPMAAINTAMNDFLGG- 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 39; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROMARYOLES
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PAPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR PAPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
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                                                                                                                                                               --- SFDINMGQASALGFEL 172
                                                                                                                                                                                          283 TIHLAGSMMKIGLFTFAVVFMYDMEVGVGLSIGFLL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534 GMVPPLAIFVATLLFKDKFTKEERNSGLTNIIMG 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                        Sequence 13341, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/09910186A Publication No. US20030009025A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13341
                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen, Kari E.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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US-09-910-186A-22
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Sequence 25, Application US/10011588

Sequence 25, Application US/10011588

Patent No. US20020168727A1

GENERAL INFORMATION:

APPLICANT: Smith, Leonard

APPLICANT: Jensen, Melody

TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM.

TITLE OF INVENTION: RESEARCH AND LIGHT CHAIN FUSION PROTEINS FOR USE IN TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY

FILE REFERENCE: A34796 067252.0113

CURRENT APPLICATION NUMBER: US/210/011,588

CURRENT APPLICATION NUMBER: US/210/010,186

PRIOR FILING DATE: 2000-07-06

PRIOR FILING DATE: 2000-07-06

PRIOR FILING DATE: 2000-01-06

PRIOR FILING DATE: 2000-11-06

PRIOR FILING DATE: 2000-11-06

PRIOR FILING DATE: 2000-11-06

PRIOR FILING DATE: 2000-11-06

PRIOR FILING DATE: 2001-10-06

PRIOR FILING DATE: 2001-10-06

PRIOR FILING DATE: 2001-10-06
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|180 IVPY-IGLALNVG-NETAKGNFENAFEIAGASILLEFIPELLIPVVGAFLLESYIDNKNK 237
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GENERAL INFORMATION;
SCHERAL INFORMATION;
TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
TITLE OF INVENTION: NEUROPOTIN
FILE REFERENCE: A3366.A 067252.0107
CURRENT EDITOR ON NEUROPOTIN
FILE REFERENCE: 2001-07-20
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: DCT/US00/12890
PRIOR PILING DATE: 2000-05-12
PRIOR PAPLICATION NUMBER: 09/611,419
PRIOR PELING DATE: 2000-05-12
PRIOR PELING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR PELING DATE: 1993-09-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic Construct
US-09-910-186A-22
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------GFLILGFDAVGIGLILTGAYLDIKALDKNAP-KAAFK---WTW----GKG 112
                                                                                                              178 GIEYSPGVGVDYWIWSLQLSGIGTTLTGINFFVTILKMRAPGMTMFKMPVFTWASLCANV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 FVIGLMNLVVPLQIGARDVAFPFLNNLSFWFTVVCVILVNLSLGVGEFAQTGWLAYPPLS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 ------GFLILGFDAVGIGLILTGAYLDIKALDKNAP-KAAFK---WTW----GKG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 GIEYSPSVGVDYWIWALQLSGIGTTLTGINFFVTILKMRAPGMTMFKMPVFTWASLCANV 237
  118 FVIGLMNLVVPLQIGARDVAFPFLNNLSFWFTVVGVILVNVSLGVGEFAQTGWLAYPPLS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                     113 MMLAG----AVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEP 156
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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8.7%; Score 78.5; Di
Best Local Similarity 22.6%; Pred. No. 3.3;
Matches 38; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TILLE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILIDE DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-36

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FASTSEQ FOI WINDOWS VERSION 4.0

SEQ ID NO 14080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(663); OTHER INFORMATION: Xaa = Any Amino Acid US-09-815-242-14080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 FNLGAGEKLLAYETSKKDPIVPFLLNLF----
                                                                                                                                                                                                                                                                                                                                                                  Sequence 14080, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                             RESULT 6
US-09-815-242-14080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               -----GIGLILTGAYLD---- 92
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                                                                                                                                                                                               ; OTHER INFORMATION: Recombinant protein encoded by SEQ ID NO:24 US-10-011-588-25
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                                                                                                                                                                                                                                                                                   Length 852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Oblisher, Kari L.
APPLICANT: Oblisher, Kari L.
APPLICANT: Wall, Dudith W.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranimoro, Robert T.
APPLICANT: Tanamoto, Robert T.
APPLICANT: Wall Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.Olf. 9.21
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/291,078
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-112-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-21-22
PRIOR FILING DATE: 2001-21-22
                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                              9.0%; Score 81.5; DB 9;
23.8%; Pred. No. 2.2;
tive 24; Mismatches 56;
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8.7%; Score 78.5; Di
Best Local Similarity 22.6%; Pred. No. 3.3;
Matches 38; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            47 IVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 -IKALDKNAPKAAFKWTWGKGMMLAGAVTMAVTRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 FNLGAGEKLLAYETSKKDPIVPFLLNLFLGF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 FANSYNRKLKNSLNIAFGGFEPSFDINMGQA 165
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10070, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                Query Match 9.0%
Best Local Similarity 23.8%
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-815-242-10070
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LENGTH: 663
                                                                                                                                                                        FEATURE:
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253 YENKIKHPLVDFSIFKNRGYSGATISNFLLNGVAGGALIVINTYYQQQLGFNSSQTGYIS 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-22
PRIOR PAPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SSOFTWARE: FESSESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.4%; Score 76; DB Best Local Similarity 26.1%; Pred. No. 3.6; Matches 29; Conservative 17; Mismatches
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 6/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-66
PRIOR FILING DATE: 2001-02-66
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASTSEQ for Windows Version 4.0
SSOFTWARE: 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Staphylococcus aureus US-09-815-242-13058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ohlsen, Kari I.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Helicobacter pylori
US-09-815-242-11462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-815-242-11462
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LENGTH: 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 411;
                                                                                                                                          APPLICANT: Obligen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tanamoto, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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APPLICANT: Obligation, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: 40-11, Daniel
APPLICANT: Tranick, John D.
APPLICANT: Tannick, John D.
APPLICANT: Tannick, Robert T.
APPLICANT: Yannamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
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8.4%; Score 76; DB 1
Best Local Similarity 26.1%; Pred. No. 3.4;
Matches 29; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/201, 178
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-11-27
PRIOR PAPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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                                Sequence 5875, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION UNBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT CAGANISM: Staphylococcus aureus US-09-815-242-5875
                                                                                           GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-09-815-242-13058
        US-09-815-242-5875
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22;

43; Indels

DB 10; Length 432;

DB 10; Length 206; 8.4%; Score 75.5; Query Match

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Best_Local Similarity 26.29
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Homo sapiens
US-09-925-637-16
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   RESULT 11
US-09-741-669-422
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                                                                                           86 GHFVQGHI------DAIGV----IEKIIHNANQVDFFISASEETLLLCVEQ 126
                                                                                                                                                         76 GFDAVGIGLILTGAYLDIKALDKNAPKAAFKWT--WGKGMMLAGAVTMAVTRLTEIIIPF 133
                                                                                                                               112 GMMLAGAVTMAVTRLTE----IIIPFTFANSYNR--KLKNSLNIAFG------- 152
                     Gaps
                     49;
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Guo-Liang
APPLICANT: Wang, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Hulbert, Scot
APPLICANT: Richter, Todd
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resisitance in Plants
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 TFAN-----SYNRKLKNSLNIAFGGFEPSFDINMGQASALGFELSFKK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              887 TFENVVRATGSFNA----SNCIGSGGFGATYKAEI----APGFLVAVKR 927
                   38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,386A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor STATE: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058950US
23.6%; Pred. No. 1.6; cive 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.1%; Score 73.5; C
28.4%; Pred. No. 22;
ative 17; Mismatches
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CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       RESULT 10
US-08-910-386A-20
Sequence 20, Application US/08910386A
; Patent No. US20020092041A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                           153 -- GFEPSFDINMGQASALGF 170
                                                                                                                                                                                                                                   187 TKGFEKNFSWNEADALTLGY 206
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Ronald, Pamela C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
Best Local Similarity 23.6%
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-910-386A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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Best Local Similarity
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94111-3834
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9
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APPLICANT: Choi
TITLE OF INFORMATION:
FILE OF INFORMATION:
CURRENT APPLICATION NUMBER: US/09/925,637
CURRENT APPLICATION NUMBER: US/09/925,637
CURRENT FILING DATE: 2001-08-10
PRIOR PLILING DATE: 1999-00-10
PRIOR FILING DATE: 1999-00-10
PRIOR FILING DATE: 1999-00-10
PRIOR PELICATION NUMBER: US 08/781,986
PRIOR PELICATION NUMBER: US 08/956,171
PRIOR APPLICATION NUMBER: US 08/956,171
PRIOR PELING DATE: 1997-01-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKNAPKAAFKW-----TWGKGMMLAGA-----VTMAVTRLTEIIIPFTFANSYNRKL 143
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Sequence 422, Application US/09741669
Fatent No. US/3002022718A1
GENERAL INFORMATION:
APPLICANT: POSSYL, R. Allyn
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: ELITRA.009A
TITLE OF INVENTION: Proliferation of E. coli
FILE REFERENCE: ELITRA.009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SEQ ID NO 422
LIENGTH: 451
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26.2%; Pred. No. 8.7;
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ilarity 21.3%; Pred. No. 9.9;
Conservative 28; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Mismatches
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SOFWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 452
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nes 37; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 FVSASDPQSIIRSEPRADRGYGRKLLA-QLNPTWPITP------IGQFALNRSVPA 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 FAQADDSKSAF-----NLGAGEKLLAYETSKKDPIVPFLLNLFLGFGIGSFAQGDIL--
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Fatent No. US20020165137A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA127P1
CURRENT FILING DATE: 2001-05-21
FILE TO TO Application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 289
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: PATENTING DATE: 100 OF 134
LENGTH: 354
TYPE: PRT

CORGANISM: HOMO Sapiens
                                                                                                                                                                                                                                                                                                                                                                                Length 292;
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26.5%; Pred. No. 6.5;
cive 18; Mismatches 56;
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Best Local Similarity 22.1%; Pred. No. 8.3;
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                    PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PLILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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ne : 12 secs
                                                                                                                                                                                                                                                                             ; TYPE: PRT; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4426
  2000-12-18
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Sequence 16, Application US/09881752A

Sequence 16, Application US/09881752A

GENERAL INFORMATION:

APPLICANT: Kleathous, Harold

APPLICANT: Al-Garawi, Amal

APPLICANT: Tomb, Jean-Francois

APPLICANT: Tomb, Jean-Francois

APPLICANT: Tomb, Jean-Francois

APPLICANT: Gomen, Raymond P.

TITLE OF INVENTION: Encoding No. US20020115078Alel Helicobacter Polypeptides in the

TITLE OF INVENTION: Genome

FILE REFERENCE: 06/13/041002

CURRENT APPLICATION NUMBER: US 08/883,457

PRIOR FILING DATE: 1997-04-01

NUMBER OF SEQ ID NOS: 370

SEQ ID NO 16

LENGTH: 220
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                                                                        ---GAYLDIKALDKNAPKA--AFKWTWGKGMMLAGAVTMAVTRLTEII 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 ALD-----KNAPKAAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSL 147
1 MNKFLIVVLLAFCVFSSFAQAD---DSKS-----AFNLGAGEKLLAYETSKKDPIV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 PFLLNLFL---GFGIGSFAQGDILGGFLILGFDAV----GIGLILT-----GAYLDIK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNKTTVKIIMGMALLSSLQAAEAELDEKSKKPKFADRNTFYLGVGYQLSAINTSFSTESV
                                                                                                                                                                        ----FTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASAL 168
                                                                                                                                                                                                       138 NPELPRPVGNDIVHYSDYFEGAQKYLSYLKSTVDVNFEGLKIALDGANGSTSSL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 220;
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APPLICANT: NAZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
APPLICANT: OYOVEL POLYNUCLEOTIDES
FILE REFERRUCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
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Publication No. US20020197605A1
GENERAL INFORMATION:
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                                                                        83 GLILT-----
                                                                                                                                                                        131 IP-----
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US-09-881-752A-16
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 protein search, using sw model OM protein March 14, 2003, 14:22:16; Search time 12.264 Seconds Run on:

(without alignments)
1387.454 Million cell updates/sec

US-09-508-487-23 908 1 MNKFLIFILVIFCAFSSFAQ......DINMGQASALGFGLSFKKSY 177 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Fotal number of hits satisfying chosen parameters:

inimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

glycosyltransferas	hypothetical prote	non-proteolytic bo	. C4-dicarboxylate t	surface-array prot	hypothetical prote	probable sugar-pro	hypothetical prote	PTS system, maltos	macrolide-efflux p	closely related to	bacterial adhesin	eae protein (enter	hypothetical prote	protein T24E12.8 [sugar transport pr
A97271	A70169	140631	D83498	A37284	в97739	H97064	T32727	D70114	н69864	н97092	I40705	141197	S73384	E88109	Н90423
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80	80	80	79.5	79.5	79	79	79	79	78.5	78.5	78.5	78.5	7.8	7.8	7.8
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ALIGNMENTS

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RESULT 1
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c; Species: By 7014
b; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; W
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; V
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; V
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Nature 390, 580-586, 1997
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; Gaps .. Length 179; Query Match 81.2%; Score 737; DB 2; Length 17' Best Local Similarity 81.0%; Pred. No. 5.5e-60; Matches 14; Conservative 14; Mismatches 18; Indels

1 MNKFLIFILVIFCAFSSFAQ-DDSKS-TFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFG 58 ŏ

g

59 IGSFAQGDILGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKADFKWTWGKGMMLAGVV 118 ò

g

119 TMAVTRLTEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177 ò g

Conserved hypothetical protein BBA01 - Lyme disease spirochete plasmid A/lp54
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Accession: A70207
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Retrason, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, J. A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Ritle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685

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                                                                                 A)Cross-references: GB:AE000790; NID:g2690224; PIDN:AAC66226.1; PID:g2690225; TIGR:BBA01A)Experimental source: strain B31 C; Genetics: Science is a specific blasmid A; Genome: plasmid C; Superfamily: Lyme disease spirochete plasmid hypothetical protein BBA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Fraser, C. M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bomman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
A.Authors: Smith, H.O.; Venter, J.C.
A.Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A.Reference number: A70100; MUID:98065943; PMID:9403685
A.Reference number: A70103
A.Rocession: F70343
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein BBI31 - Lyme disease spirochete plasmid I/1p28-4 C.Species: Borrelia burgdorferi (Lyme disease spirochete) C.bate: 11-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 17-Mar-2000 C.Accession: F70243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-161 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                               SFAQGDILGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKADFKWTWGKGMMLAGV-VT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFAQGDILGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKADFKWTWGKGMMLAGVVTM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 SFVQGDYIGGGAVLGSQLLGGILCIAGNILGHTDDETRA-----TTGHIITTIGVGTI 118
                                                                                                                                                                                                                                                                                                                                                                           1 MNKFLIFILVIFCAFSSFAQDDSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFGIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNKFLIFILVIFCAFSSFAQDDSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFGIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAVTRLT-EIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AVTRLIEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 IASHIASLIIPFTFANKHNANLKKRLGIDIAGFEPNFDIGIS-----GFQLSFKKRY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome: plasmid
Superfamily: Lyme disease spirochete plasmid hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.2%; Score 301.5; DB 2; Length 170; llarity 40.1%; Pred. No. 2.5e-20; Conservative 23; Mismatches 70; Indels 13
                                                                                                                                                                                                                                             Length 161;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                             60;
                                                                                                                                                                                                                                        34.0%; Score 309; DB 2;
41.3%; Pred. No. 4.9e-21;
tive 25; Mismatches 60)
                                                                                                                                                                                                                                      Query Match 34.0%
Best Local Similarity 41.3%
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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Authors: Smith, H.O.; Venter, J.C.
Ayathors: Genomic sequence of a Lywe disease spirochaete, Borrelia burgdorferi.
Ayacession: G70239
Aystatus: preliminary; nucleic acid sequence not shown; translation not shown
Ayathorial evolue type: DNA
Ayathors: 1-190 <ALE>
Ayathors: 1-190 <ALE>
Ayathors: 1-190 <ALE>
Ayathors: 1-190 <ALE>
Ayathors: 1-190 <ALE>
Ayathors: 1-190 <ALE>
Ayathors: 1-190 <ALE>
Ayathorian and Surce: Strain B31
Ayathorian source: strain B31
C; Superimental source: strain B31
C; Superfamily: Lyme disease spirochete plasmid hypothetical protein BBA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP dependent helicase homolog lin0195 [imported] - Listeria innocua (strain Clip1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
Nature 390, 580-586, 1997
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A;Cross-references: GB:AL592022; PIDN:CAC95428.1; PID:g16412614; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 DILGGSLILGFDAVGIGLILTGAYLD-IKDFDNNAKKADFKWTWGKGMMLA-----GVV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      668 VDLRGERLIGTAIVGVGLAQMNVESDLIKDYYNE-----TIGRGFDYAYQIPGMNKV 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 FDNNAKKADFKWTWGKGMMLAGVVTMAVTRLTEIVLPFTFANNYNRKLKNSLNIALGGFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 AFSSFAQ------DDSKSTFNLGAGEKFL-VYETNKKDSLVPFLLNLFLGFGIGSFAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 TMAVTRLTE-----IVLPFTFAN------NYNRKLKNSLNI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%; Score 93; DB 2; Length 779; 26.6%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 26.4%; Score 240; DB 2;
Local Similarity 41.3%; Pred. No. 1.1e-14;
Hes 59; Conservative 22; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 PNLDIGMN----GFOLSFKKSY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 PSFDINMGQASALGFGLSFKKSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 26.6
nes 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: lin0195
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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LVPFLLNLF - - - LGFGIGSFAQGDILGGSLILGFDAVGIGLILTGAYLD -
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Best Local S
Matches 30
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              probable sugar ABC transporter permease protein SMb20315 [imported] - Sinorhizobium melifical Cispecies: Sinorhizobium meliloti C.Sate: S4-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C:Accession: E55879  
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A;Accession: E95879
                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-376 < KURS
A; Residues: 1-376 < KURS
A; Residues: 1-376 < KURS
A; Cross-references: GB:AL591985; PIDN:CAC48701.1; PID:g15140174; GSPDB:GN00167
A; Experimental source: strain 1021, megaplasmid pSymB
B; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pelan, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Science 293, 668-672, 2001
A; Althors: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Pabault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphotransferase system enzyme II, galactitol specific, protein C - Escherichia coli C; Species: Escherichia coli A; Variety: strain EC3132
A; Variety: strain EC3132
C; Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 29-Sep-1999
C; Accession: 555905; 549083
R; Nobelmann, B.; Lengeler, J.W.
Biochim: Biophys. Acta 1262, 69-72, 1995
A; Reference of the gat operon for galactitol utilization from a wild-type strain A; Reference onumber: 555901; WUID:95290497; PMID:7772602
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A;Molecule type: DNA
A;Residues: 1-427 <NOB>
A;Cross-references: EMBL:X79837; NID:9599737; PIDN:CAA56230.1; PID:9508175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFAQGDILGGSLILGFDAVGIGLIL---TGAYLDIKDFDNNAKKAD--FKWTWGKGMMLA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GV-----VIMAVTRLTEIVLPF---TFANNYNRKLKNSLNIALGGFEPSFDINMGQAS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 MIAGGG------GIDLSGIALANLAGVGSYLLVRDW-VSADEAPLAFSWLFAAMALLI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 376;
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C;Superfamily: phosphotransferase enzyme II galactitol-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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1.5;
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26.1%; Pred. No. 1.5;
Live 19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 26.19
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 : |
216 VLGVPMCF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 ALGFGLSF 173
                                                                                                                                                                                                                                 A; Status: preliminary
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A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change Ol-Mar-2002
C;Accession: C64976
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-451 <BLAT>
A;Residues: 1-451 <BLAT>
A;Residues: 1-451 <BLAT>
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTS system galactitol-specific enzyme IIC [imported] - Escherichia coli (strain 0157 C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. Accession: G90900
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Han, Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Actaus: preliminary
A; Molecule type: DNA
A; Residues: 1-451 < HAX>
A; Residues: 1-451 < HAX>
A; Cross-references: GB:BA000007; PIDN:BAB36318.1; PID:g13362364; GSPDB:GN00154
A; Experimental source: strain O157:H7, substrain RIMD 0509952
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9
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---IK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVPFLLNLF---LGFGIGSFAQGDILGGSLILGFDAVGIGLILTGAYLD-----IK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 LVPFLLNLF---LGFGIGSFAQGDILGGSLILGFDAVGIGLILTGAYLD-----IK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
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                                                                                                                                                                      A;Gene: gatC
C;Superfamily: phosphotransferase enzyme II galactitol-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 DFDNNAKKADFKW-----TWGKGMMLAGV-----VTMAVTRLTEIV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: ECs2895
C;Superfamily: phosphotransferase enzyme II galactitol-specific
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                                                                                                                                 DFDNNAKKADFKW-----TWGKGMMLAGV-----VTMAVTRLTEIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 9.7%; Score 88.5; DB Local Similarity 27.5%; Pred. No. 1.8; es 30; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                              gatC protein - Escherichia coli (strain K-12)
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Wernare tetanus

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A Molecule type: mRNA
A; Residues: 1-313, 'S', 315-451 < KUR>
A; Residues: 1-313, 'S', 315-451 < KUR>
A; Experimental source: strain Okra
A; Note: sequence extracted from NCBI backbone (NCBIP:109365)
B; DasGupta, B.R.; Datta, A.
B; DasGupta, B.R.; Datta, A.
B; DasGupta, B.R.; Datta, A.
B; DasGupta, B.R.; Datta, A.
B; DasGupta, B.R.; Datta, A.
B; DasGupta, B.R.; Datta, A.
B; DasGupta, B.R.; Datta, A.
B; DasGupta, B.R.; Datta, A.
B; DasGupta, B.R.; Datta, A.
B; DasGupta, B.R.; Datta, A.
B; DasGupta, B.R.; Datta, A.
B; DasGupta, B.R.; DasG
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A) Molecule type: protein
A) Molecule type: protein
A) Molecule type: protein
A) Molecule type: protein
B) Molecule type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein type: protein typ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2 C; Superfamily: tetanus toxin C; Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc F; 2441/Product: bontoxilysin B light chain #status experimental <LGHT> F; 442-1291/Product: bontoxilysin B heavy chain #status experimental <HVV> F; 230, 234/Aluding site: zinc (His) #status predicted F; 231/Active site: Glu #status predicted
                                            A,Cross-references: EMBL:211934; NID:940383; PIDN:CAA77991.1; PID:940384
R;Kurazono, H.; Mochida, S.; Binz, T.; Eisel, U.; Quanz, M.; Grebenstein, O.; V
J. Biol. Chem. 267, 14721-4729, 1992
A;Title: Minimal essential domains specifying toxicity of the light chains of A;Reference number: A42871; MUID:92340509; PMID:1634516
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A; Residues: 442-463, R', 465-467 <DA2>
R; Residues: 442-463, R', 465-467 <DA2>
R; Schmidt, J.J.; Sathyamoorthy, V.; DasGupta, B.R.
Arch. Biochem. Biophys. 238, 544-548, 1985
A; Title: Partial amino acid sequences of botulinum neurotoxins types B
A; Reference number: S07128; MUID:85197963; PMID:3888113
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Best Local Similarity 22.8%; Pred. No. 7.5;
Matches 38; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown
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A;Residues: 2-29,'M',31-45 <DAS>
A;Accession: S08562
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A; Residues: 2-16 <SCH1>
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A:Cross-references: GB:M81186; NID:g144734; PIDN:AAA23211.1; PID:g144735
A:Experimental source: type B, Danish
A:Experimental source: type B, Danish
A:Experimental source: type B, Danish
A:Experimental source: type B, Danish
A:Experimental source: type B, Danish
A:Experimental source: type B, Danish
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A:Experimental source: type B, Danish
A:Experiment
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; Molecule type: DNA
; Residues: 1-451 <STO>
A; Cross-references: GB: AE005174; NID: g12516295; PIDN: AAG57149.1; GSPDB: GN00145; UWGP: Z3Z
A; Experimental source: strain 0157: H7, substrain EDL933
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C;Accession: A48940; S48105; S21575; A42871; S07155; S08562; S07128; S08573; S08574
Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P.
Ppl. Environ. Microbiol. 58, 2345-2354, 1992
A;Title: Molecular cloning of the Clostrialium botulinum structural gene encoding the transference number: A48940; MUID:92384550; PMID:1514783
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A; Residues: 634-994 ccAM>
A; Residues: 634-994 ccAM>
A; Residues: 634-994 ccAM>
A; Cross references: EMBL:X70817; NID:g407782; PIDN:CAA50148.1; PID:g407783
A; Experimental source: proteolytic type B, strain NCTC 7273
B; Szabo, E.A.; Pemberton, J.M.; Desmarchelier, P.M.
submitted to the EMBL Data Library, April 1992
A; Description: Partial amino acid sequence of botulinum neurotoxin type B and A; Reference number: S21575
A; Accession: S21575
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                                                                                        bontoxilysin (EC 3.4.24.69) B precursor - Clostridium botulinum N;Alternate names: botulinum neurotoxin type B (BoNT/B) C;Species: Clostridium botulinum
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27.5%; Pred. No. 1.8
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DFDNNAKKADFKW---
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tes 30; Conserv
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A; Molecule type: DNA
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C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C;Accession: JC5041; F64778
Es:Fujisaki, S:; Ohnuma, S:; Horiuchi, T.; Takahashi, I.; Tsukui, S.; Nishimura, Y.;
Gene 175, 83.87, 1996
A;Title: Cloning of a gene from Escherichia coll that confers resistance to fosmidom
A;Reference number: JC5041; MUID:97074653; PMID:8917080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Rolecule type: DNA A;Rosidues: 1-406 <BLAT> A;Cross-references: GB:AE000154; GB:U00096; NID:g1786683; PIDN:AAC73581.1; PID:g1786 C;Genetics:
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A; Accession: JG5041
A; Molecule type: DNA
A; Rosidues: 1.406 <FUJ>
A; Rosidues: 1.406 <FUJ>
A; Rosidues: 1.406 <FUJ>
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A; Rosidues: 1.406 <FUJ>
A; Rosidues: 1.406 <FUJ>
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue A; Rosidue 
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                                                                                                                                                                                                                                                                                                                                               fosmidomycin resistance protein - Escherichia coli (strain K-12)
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C; Superfamily: fosmidmycin resistance protein
C; Keywords: antibiotic resistance; transmembrane protein
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23.2%; Pred. No. 2.7;
tive 27; Mismatches
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              FTFANNYNRKL 142
                                                                                                       181 FLLVQEKGKKV 191
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C;Species: Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-2000
C;Accession: H75011
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Recession: H75011
A;Status: preliminary
A;Mocession: H75011
A;Mocession: H75011
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A; Molecule type: DNA
A; Residues: 1.389 <SAM>
A; Cross-references: EMBL:U64851; PIDN:AAC47989.1; GSPDB:GN00023; CESP:F28A12.4
A; Experimental source: strain Bristol N2; clone F28A12
C; Genetics:
A; Genetics:
A; Map position: 5
A; Introns: 104/2; 147/3; 175/3; 258/3; 301/3; 341/3
hypothetical protein F28A12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C;Aatession: T28954
R;Sammons, L.; Murray, J.
Submitted to the EMBL Data Library, July 1996
A;Beference number: 220547
A;Reference number: 220547
A;Reference number: 220547
A;Reference number: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57; Indels
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Matches 40; Conservative
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A, Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gend A. Reference number: A99629; MUID:21156231; PMID:11258796
A. Accession: D90695
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-406 < HAV>
A. Residues: 1-406 < HAV>
A. Experimental source: strain 0157:H7, substrain RIMD 0509952
C. Genetics: C. Genetics: A. Genetics: C. Strain resistance protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 DILGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKADFKWTWCKGMMLAGVVTWAVTRL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
9.5%; Score 86; DB 2; Length 406;
Best Local Similarity 23.2%; Pred. No. 2.7;
Matches 39; Conservative 27; Mismatches 64; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            6 IFILVIFCAFSSFAQDDSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFGIGSFAQG 65
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GenCore version $5.1.4_p5_4578$ Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

March 14, 2003, 14:21:36; Search time 7.29214 Seconds (without alignments) 1006.744 Million cell updates/sec Run on:

US-09-508-487-23 908 1 MNKFLIFILVIFCAFSSFAQ......DINMGQASALGFGLSFKKSY 177 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

inimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P37189 escherichia				O66932 aquifex aeo	P36091 saccharomyc						Q07591 citrobacter		P75596 mycoplasma			-	Q9za21 haemophilus		P04845 serratia ma	P36845 human adeno		Q9zkd0 helicobacte		Q05233 mycobacteri	-	Q9cgi8 lactococcus					22	Q00766 dictyosteli
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ALIGNMENTS

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us-09-508-487-23.rsp

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                     Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Handa T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 015:17 and genomic comparison with a laboratory strain K-12."; DNA Res. B.11-22(2001).
                                                                                                                                                                                                             SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE LICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHORHER); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFIKQEKVVLAE -> TGRFSHYLVTDSGFSPQIFPVSLLS
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                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane. SIMILARITY: CONTAINS 1 PTS EIIC DOMAIN.
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MGPIAVLVDAILEKIPG -> LGPNCGAGGCYHRENPS
 "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
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InterPro; IPR004703; Gal_spec_IIC.
InterPro; IPR004703; Gal_spec_IIC.
InterPro; IPR004703; Gal_spec_IIC.
IIGRPAMS; TIGG0827; EliC-GAT; 1.
Phosphotransferase system; Sugar transport; Transmembrane; Inner membrane; Galactitol metabolis; Complete protecome.
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                                          SEQUENCE FROM N.A.
STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
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DEBUTIFICATION OF SUBSTRATE.

MEDLINE=3063293; bubMed=1331807;

A Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,

B schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,

Dasgupta B.R., Montecuco C.;

"Tetanus and botulinum-B neurotoxins block neurotransmitter release
by proteolytic cleavage of synaptobrevin.";

L. Nature 359:832-835(1992).

-1- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

RELEASE. IT BINDS TO PERIPHERAL SYNAPSES, IS INTERNALIZED

AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD

WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT

INHIBITS NEURORRANSMITTER RELEASE BY ACTING AS A ZINC

ENDOPERTINASE THAT CLEAVES THE 76-GLN-|-PHE-77 BOND OF

SYNAPTOBREVIN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94013372; PubMed-8408542; Campbell K., East A.K., Collins M.D.; Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F."; J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schiavo G., Rossetto O., Santucci A., Dasgupta B.R., Montecucco C.; "Botulinum neurotoxins are zinc proteins.";
                                                                                                                                                                                                                                                                        MEDLINE-92384550; PubMed-1514783; Whelan S.M., Elmore M.J., Bodsworth N.J., Brehm J.K., Atkinson T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.; "Partial amino acid sequences of botulinum neurotoxins types B and
                                                                                                                                                         Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                               "Molecular cloning of the Clostridium botulinum structural gene encoding the type B neurotoxin and determination of its entire nucleotide sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dasgupta B.R., Datta A.;
"Botulinum neurotoxin type B (strain 657): partial sequence and
BXB_CLOBO STANDARD; PRT; 1290 AA. p1084; p1084; p10843; 01-JUL-1989 (Rel. 11, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Botulinum neurotoxin type B precursor (EC 3.4.24.69) (BONT/B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Szabo E.A., Pemberton J.M., Desmarcheller P.M.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                   Appl. Environ. Microbiol. 58:2345-2354(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tulinum neurotoxins are zinc proteins.";
Biol. Chem. 267:23479-23483(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arch. Biochem. Biophys. 238:544-548(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89000987; PubMed=3139097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=OKRA;
MEDLINE=85197963; Pubmed=3888113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION AS ZINC-PROTEASE. MEDLINE=93054694; PubMed=1429690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 633-993 FROM N.A. STRAIN=NCTC 7273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-44 AND 441-466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-16 AND 441-458.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 35-245 FROM N.A. STRAIN-NCTC 7273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochimie 70:811-817(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity with tetanus
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                  NCBI_TaxID=1491;
                                                                                                                     (Bontoxilysin B)
                                                                                                                                                                                                Clostridium.
                                                                                                                                                                                                                                                                                                                Minton N.P.;
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EMBL;
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                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
         neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAV CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 VVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYK 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYETNKKDS-----LVPFL---LNLFLGFGIGSFAQG-DILGGSLILGFD----AV 79
                                                                                  MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                                                                                                                                                                                                                                                                                                                                               BOTULINUM NEUROTOXIN B, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN B, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 GIGLILTGAYLD----IKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
                                                                                                                                                                                                                                                                                                                                                                                   Probom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
INIT_MET 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 87; DB 1; Length 1290; Pred. No. 3.6;
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T -> M (IN REF. 4).

R -> G (IN REF. 2).

A -> S (IN REF. 2).

S -> R (IN REF. 4).

MM; D21746E2C024DF43 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           BOTULINUM NEUROTOXIN ZINC (CATALYTIC) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
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                                                                         SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00760; BONTOXILYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.6%;
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1290
229
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233
233
217
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463
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S08574; S08574.
A48940; A48940.
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                                                                                                                                                                                                                                                      S07128; S07128.
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463
1290
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MEROPS; M27.00
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METAL
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ID FSR_E
AC P5206
DT 01-0C
                                                                                                                                                                                                                                                                                                            PIR;
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                                                                                                                                                                                                                                                                                                         Fujisaki S., Ohnuma S.-I., Horiuchi T., Takahashi I., Tsukui S., Nishimura Y., Nishimura Y., Kitabatake M., Inokuchi H.; "Cloning of a gene from Escherichia coli that confers resistance to fosmidomycin as a consequence of amplification."; Gene 175:83-87(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDILINE-97426617; PubMed-9278503;
MEDILINE-97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett S. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Rirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 IFILVIFCAFSSFAQDDSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFGIGSFAQG
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Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: CONFERS THE RESISTANCE AGAINST FOSMIDOMYCIN.
                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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Pred. No. 1.4:
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
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MEDLINE-97074653; PubMed-8917080;
                                                     Fosmidomycin resistance protein.
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EMBL; AE000154; AAC73581.1; -
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ne; EG13268; fsr.
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Matches 39; Conserv
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                           Escherichia coli
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                                                                                  FSR OR B0479
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SEQUENCE
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RA KUIBE F., OGGGGWARTA N., MOSSET I., Albertini A.M., Alloni G.,

RA Acevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouilet S., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Entian K.D., Errington J., Fabret C., Harloch S.D., Emmerson P.T.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Coris B., Karamata D., Kasabara Y., Klaerr-Blanchard M., Klein C.,

A Kutita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Kubayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kudita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Resecan E., Pujic P., Purnelle B., Roche B., Park S.H.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

Schiguchi J., Sckowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Tanamoto H., Vannier F., Vassarotti A.,

RA Takeuchi M., Tamakoshi A., Tanamoto H., Vanner F., Vassarotti A.,

RA Takeuchi M., Tamamakoshi A., Tanamance H., Waltzenegger T.,

RA Viari A., Wambutt R., Wadler E., Waller H., Waltzenegger T.,

RA Takeuchi M., Tamamoto H., Yamane K., Yasumoto K., Yata K.,

RA Viari A., Wambutt R., Wandeler E., Waller H., Washikawa H., Danchin A.,

The Complete genome sequence of the Gram-positive bacterium Bacilus

RY Subtils.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "New genes in the 170 degrees region of the Bacillus subtilis genome encode DNA gyrase subunits, a thioredoxin, a xylanase and an amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schloett T., von Wachenfeldt C., Hederstedt L.;
"Identification and characterization of the ccdA gene, required for eytochrome c synthesis in Bacillus subtilis.";
J. Bacteriol. 179:1962-1973(1997).
                                                    323 --VIIGFILASAFSAILVYAQELLPG------RIGMVSGLFFGFAF 360
                   TEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQASALGFGLSF 173
                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Cytochrome c-type biogenesis protein ccdA.
                                                                                                                                                                                                        235 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98044033; PubMed-9384377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microbiology 142:3097-3101(1996)
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01-NOV-1995 (Rel. 32, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 LFLGFGIGSFAQGDI------LGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 DF------KWIWGKGMMLAGVVTMAVTR------LTEIVLPFTFANNYN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                            protein.";
J. Bacteriol. 182:2845-2854(2000).

-I- FUNCTION: REQUIRED FOR CYTOCHROME C SYNTHESIS AND STAGE V OF SPORULATION. MIGHT TRANSFER REDUCING EQUIVALENTS ACROSS THE CYTOPLASMIC MEMBRANE, PROMOTING EFFICIENT DISULFIDE BOND ISOMERIZATION OF PROTEINS LOCALIZED ON THE OUTER SURFACE OF THE
                         Schioett T., Hederstedt L.; {\tt ^{\rm 2}} {\tt ^{\rm 2}} Efficient spore synthesis in Bacillus subtilis depends on the CcdA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 FLSFISPCCLPLYPAFLSYITGVSMDDVKT-----EKLLLQKRSLFHTLC-FLLGFSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytochrome c-type biogenesis; Sporulation; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65; Indels
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D94F3E62EDD2AC29 CRC64;
                                                                                                                                                                                                                                       MEMBRANE OR IN THE SPORE COAT.
-!- PATHWAY: CYTOCHROME C SYNTHESIS SYSTEM II.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE DSBD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Glycogen phosphorylase (EC 2.4.1.1). GLGP OR AQ_717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.4%; Score 85; DB Local Similarity 24.4%; Pred. No. 0.95 les 48; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
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MEDLINE=20245543; PubMed=10781554;
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77 PC
1107 PC
1153 PC
1153 PC
224 PC
26007 MW;
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066932;
30-MAY-2000 (Rel. 39, Created)
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NCBI_TaxID=63363;
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STRAIN=S288c;
MEDLINE=94205268; PubMed=8154189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                  FUNCTION: PHOSPHORYLASE IS AN IMPORTANT ALLOSTERIC ENZYME IN CARBOHYDDARTE METRABOLISM. ENZYMES FROM DIFFERENT SOURCES DIFFER IN THEIR REGULATORY MECIRANISMS AND IN THEIR NATURAL SUBSTRATES. HOWEVER, ALL KNOWN PHOSPHORYLASES SHARE CATALYTIC AND STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 FISHFKYVYSLYKTYMNRHSK------YEDTYKKPIV-FLSPEYGLHHTLLIY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- DFDNNAKK----- 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00343; phosphorylase; 1.
PROSITE; PS00102; PHOSPHORYLASE; 1.
Transferase; Glycosyltransferase; Carbohydrate metabolism;
Glycogen metabolism; Pyridoxal phosphate; Complete proteome.
BINDING 586 586 586 S86 S86 S86 S86 S86 S80 SEMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ADFKWTWGKGMMLA-----GVVTMAVTRLTEIVLPFTFANN--YNRKLKNSLNIA
                                      Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Carbam D.E., Overbeek R., Snead M.A., Keller M., Adjay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                 PROPERTIES (BY SIMILARITY).

CATALYTIC ACTIVITY: {(1,4)-alpha-D-glucosyl}{(N) + phosphate (1,4)-alpha-D-glucosyl}{(N-1) + alpha-D-glucose 1-phosphate. COPACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

SIMILARITY: BELONGS TO THE GLYCOGEN PHOSPHORYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ol-vow-1994 (Rel. 29, Last sequence update)
01-NOW-1997 (Rel. 35, Last annotation update)
Hypothetical 49.6 kDa protein in ELMI-PRI2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.4%; Score 85; DB 1; Length 692; 22.9%; Pred. No. 2.9; tive 28; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGFGIGSFAQGDILGGSLILGFDAVGIGLILTGAYLDIK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                        MEDLINE=98196666; PubMed=9537320;
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(Rel. 29, Last sequ
(Rel. 35, Last anno
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                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000704; AAC06896.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000811; GT_35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                    Nature 392:353-358(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    P00489; 3AMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
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01-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKE6_YEAST
P36091;
                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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YKE6_YEAST
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                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 VGIGLILTGAYLDIKD----FDNNAKKADFKWTWGKGMMLAGVVTMAVTRLTEIVLPFTF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Purnelle B., Tettelin H., van Dyck L., Skala J., Goffeau A.;
"The sequence of a 17.5 kb DNA fragment on the left arm of yeast chromosome XI identifies the protein kinase gene ELM1, the DNA primase gene PRI2, a new gene encoding a putative histone and seven new open reading frames.";
Yeast 9:1379-1384(1993).
-:- SIMILARITY: TO YEAST YMR238W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gissi C., Gullberg A., Arnason U.; "The complete mitochondrial DNA sequence of the rabbit, Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 50:161-169(1998).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DECFE9CAFD9579D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 6 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.2%; Score 83.5; D
28.8%; Pred. No. 2.5;
Live 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; S37867; S37867.
SGD; S0001529; YKL046C.
InterPro; IPR005198; Glyco_hydro_76.
Pfam; PF03663; Glyco_hydro_76; I.
Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X71621; -; NOT_ANNOTATED_CDS
EMBL; Z28046; CAA81881.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98317530; PubMed-9653643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit). Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 AA; 49565 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56
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                                                                                                                                                             7;
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                                                                                                                                                                                                                                                                                                                   63 MLVVFGYTTAMATEEYPETWGSNVMILGMFVLGVLMEVGLVVYMVMSDGVEIVVDFKNMG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILGGSLILGFDAVGIG-----LILTGAYLDIKDFDNNAKKADFK--WTWGKGMMLAGVV 118
                                                                                                                                                                                                                                                                               89 YLDIKDFDNNAKKADFKWTWGKGMMLAG------VVTMAVTRLTEIVLPFTFAN 136
                                                                                                                                                               42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 VPFLLNL-----FLGF------GIGSFAQGDILGGSLILGFDAVGIG----LILTGA 88
                                                                                                                                                                                                                                        4 VVFLLSVMFVMGFVGFSSKPSPIYGGLGLIVSGGV-GCGIVLSFGGSFLGLMMFLIYLGG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Octopine and nopaline oxidases from Ti plasmids of Agrobacterium tumefaciens: molecular analysis, relationship, and functional characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 176:4511-4517(1994).
-!- FUNCTION: OXIDATIVE CLEAVAGE OF OCTOPINE INTO L-ARGININE AND PYRUVATE (BY SIMILARITY).
-!- PATHWAY: CATABOLIC UTILIZATION OF OCTOPINE.
-!- SUBUNIT: HETERODIMER OF A SUBUNIT AND A B SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Opine oxidase subunit B (EC 1.....) (Octopine oxidase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zanker H., Lurz G., Langridge U., Langridge P., Kreusch D., Schroeder J.;
                                                                                                                     8.9%; Score 81; DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Indels
                                                                                                                                                           54; Indels
EMBL; AJ001588; CAA04858.1; -.
InterPro; IPR001457; Oxidored_q3.
Pfam; PP00499; oxidored_q3: 1.
Oxidoreductase; NAb.; Ubiquinone; Mitochondrion.
SEQUENCE 174 AA; 18728 MW; 18740BB6661D09E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Plasmid.
SEQUENCE 371 AA; 39939 MW; 948705136822AC52 CRC64;
                                                                                                                                                                                                                                                                                                                                                          137 NYNRKLKNSLNIALGGFEPSF--DINMGQASALGFG 170
                                                                                                                                                                                                                                                                                                                                                                                  :: : | | : :| | : :| | 123 DW------VVFEGDEVGLIREDSMGVAALYSYG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 AA.
                                                                                                                                       Pred. No. 1.6;
                                                                                                                                                           24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.9%; Score 81; DB 27.3%; Pred. No. 3.5; tive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agrobacterium tumefaciens (strain Ach5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000927; D_aa_oxidase.
InterPro; IPR000205; NAD_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-94321320; PubMed-8045881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z30328; CAA82987.1; -.
                                                                                                                                       23.1%;
                                                                                                                                       Local Similarity 23.1%
nes 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01266; DAO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=176298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pTiAch5
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                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10884043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Golter S.L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      opportunistic pathogen.";
Nature 406:959-964(2000).
-!- FUNCTION: Responsible for the transport of dicarboxylates such as succinate, fumarate, and malate from the periplasm across the inner membrane (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                         63 LWSDASARRWPTMANTLLDDSGIDVGLQQDGAFTFALSEEELEANRQDMESIELETNGRA 122
 ----TMAVTRLTEIVL-----PFTFANN----YNRKLKNSLNIALGGFE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (By similarity).
-!- SIMILARITY: BELONGS TO THE-SODIUM:DICARBOXYLATE SYMPORTER FAMILY (SDF, TC 2.A.23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00713; NA_DICARBOXYL_SYMP_1; FALSE_NEG.
PROSITE; PS00714; NA_DICARBOXYL_SYMP_2; 1.
Transport; Sugar transport; Transmembrane; Inner membrane; Symport;
                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCA564DB31A5AC07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 79.5; DB 1;
Pred. No. 5.6;
                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C4-dicarboxylate transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. POTENTIAL.
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POTENTIAL.
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                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001991; Na/diCO_symp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45993 MW;
                                                                    155 PSFDINMGQAS---ALGFG 170
                                                                                                    123 POFEVLDROOTLDRVLGIG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE004548; AAG04572.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00173; EDTRNSPORT
                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00375; SDF; 1
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189
226
226
327
354
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                                                                                                                                                                                                                                                                                              DCTA OR PA1183
                                                                                                                                                                                            DCTA_PSEAE
0914F5;
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RESULT 10

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935 AA
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MEDLINE-98187918; Pubmed-9529069;
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InterPro; IPR00334; Big_1.
InterPro; IPR003343; Big_2.
InterPro; IPR003535; Intimin.
InterPro; IPR002482; LysM.
Pfam; Pr02368; Big_1.
Pfam; Pr02368; Big_1.
Pfam; Pr02369; Big_1.
Prinrs; Pr01369; INTIMIN.
SMART; SM00257; LysM; 1.
Outer membrane; Virulence.
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.6%
Best Local Similarity 21.7%
Matches 34; Conservative
                                                                                                                     Escherichia coli Olll:H-.
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               STANDARD;
                                                                                                                                                                NCBI_TaxID=168927;
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Q07591;
              EAE_EC011
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EAE_CITFR
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                             DDSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAV- 79
                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90354448; PubMed=2387868;
Blaser M.J., Gotschlich E.C.;
"Surface array protein of Campylobacter fetus. Cloning and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 933;
24; Indels
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                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 30, Last annotation update)
5-layer protein (Surface array protein) (SAP)
Mismatches
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24.4%; Pred. No. 12;
Live 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 1-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                         structure.";
J. Biol. Chem. 265:14529-14535(1990).
7;
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Best Local Similarity 24.4'
Matches 33; Conservative
 Conservative
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                                                                                                                                                                                               STANDARD;
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                                                          114 DTSKIAAYAAAGE---
                                                                                                                                                                                                                                                                                                     Campylobacter fetus
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-84-32 / 23D;
                                                                                                                  162 GYALHRLGSY 171
                                                                                       GIGLILTGAY 89
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-196;
26;
                                                                                                                                                                                             SLAP_CAMFE
P35827;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infect. Immun. 66:1467-1472(1998).
-!- FUNCTION: NECESSARY FOR THE PRODUCTION OF ATTACHING AND EFFACIN LESIONS ON TISSUE CULTURE CELLS. BELIEVED TO MEDIATE ADHERENCE.
-!- SUBCELLULAR LOCATION: OUTER SURFACE.
-!- SIMILARITY: BELONGS TO THE INTIMIN/INVASIN FAMILY.
-!- SIMILARITY: CONTAINS 1 LYSM REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Voss E., Paton A.W., Manning P.A., Paton J.C.; "Molecular analysis of Shiga toxigenic Escherichia coli Olll:H-proteins which react with sera from patients with hemolytic-uremic syndrome.";
                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
110-OCT-2001 (Rel. 40, Last annotation update)
1011,111 (Attaching and effacing protein) (Eae protein).
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Intimin (Attaching and effacing protein) (Eae protein).
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P75596;
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                                                                                                                                                                                                                                            Actions—35.737, courses occord.

Schauer D. B., Falkow S.;

"Attaching and effacing locus of a Citrobacter freundii biotype that causes transmissible murine colonic hyperplasia.";
Infect. Immun. 61:2486-2492(1993).

-I. FUNCTION: NECESSARY FOR THE PRODUCTION OF ATTACHING AND EFFACING LESIONS ON TISSUE CULTURE CELLS. BELIEVED TO MEDIATE ADHERENCE.
-I. SIMILARITY: BELOAGTON: OUTER SURFACE.
-I. SIMILARITY: CONTAINS 1 LYSM REPEAT.
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                                                                Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Escherichia.
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Intimin (Attaching and effacing protein) (Eae protein).
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                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=93273499; PubMed=8500884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR003344; Big_1.
InterPro: IPR003343; Big_2.
InterPro: IPR003343; Big_2.
InterPro: IPR003482; LysM.
Pfam; Pr01476; LysM; 1.
Pfam; Pr02368; Big_2.; 1.
Pfam; Pr02369; Big_1.; 2.
PRINTS; PR01369; INTIMIN.
Outer membrane; Virulence.
REPEAT 65 113 LY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L11691; AAA23097.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=0127:H6 / E2348/69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli 0127:H6
                                 Citrobacter freundii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 936 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=168807;
                                                                                                                            NCBI_TaxID=546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAE OR EAEA.
                                                                Bacteria, Pr
Citrobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
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P19809;
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ID EAE_F
DT 01-P1
DT 01-F1
DT 01-F1
DT 01-F2
DT 02-F2
DT 03-F3
DT 03-F3
DT 01-F3
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                                                                                                                                                                                        STRAIN-0127:H6 / E2348/69;
STRAIN-0127:H6 / E2348/69;
STRAIN-0127:H6 / E2348/69;
STRAIN-0127:H6 / E2348/69;
STRAIN-0127:H6 / E2348/69;
STRAIN-0127:H6 / E2348/69;
Eliott S.J. Wainwright L.A., McDaniel T.K., Jarvis K.G., Deng Y.K.,
Lai L.C., McNamara B.P., Donnenberg M.S., Kaper J.B.;
The complete sequence of the locus of enterocyte effacement (LEE)
from enteropathogenic Escherichia coli E2348/69.";
Mol. Microbiol. 28:1-4(L998).
-: FUNCTION: NECESSARY FOR THE PRODUCTION OF ATTACHING AND EFFACING
LESIONS ON TISSUE CULTURE CELLS. BELIEVED TO MEDIATE ADHERENCE.
-: SUMCELLUAR LOCATION: OUTER SURRACE.
-: SIMILARITY: BELONGS TO THE INTIMIN/INVASIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 DSRFTANLGAGQRF------FLPENMLGYNV--FIDQDFSGDNTRLG---- 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 GLILTGAYLDIKDFDNNAKKADFKWT-WGKGMMLAGVVTMAVTRLTEIVLPFTFANNYNR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KKDYDE 324
Jerse A.E., Yu J., Tall B.D., Kaper J.B.; "A genetic locus of enteropathogenic Escherichia coli necessary for
                                                                   the production of attaching and effacing lesions on tissue culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102410 MW; 783C53EB0322DE4D CRC64;
                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 87:7839-7843(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 KLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypochetical protein MPN096 (R02_orf264).
MPN096 OR MP058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 AA.
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21.7%; Pred. No. 15;
Live 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYSM.
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InterPro; IRR003344; Big_1.
InterPro; IRR003343; Big_2.
InterPro; IRR003355; Intimin.
InterPro; IRR001304; Lectin_C.
InterPro; IRR002482; LysM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M58154; AAA62775.1; -
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Pfam; PF01476; LysM; 1.
Pfam; PF02368; Big__2; 1.
Pfam; PF02369; Big__1; 2.
PRINTS; PR01369; INTIMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00257; LysM; 1.
Outer membrane; Virulence.
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rch completed: March 14, 2003, 14:24:59 time: 10.2921 secs
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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9
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                                                                                                                                                                                                                                                                                                                                                                                                               GIGSFAQGDILG-GSLILGFDAVGI----GLILTGAYLDIKDFDNNAKKADFKWT-WGKG 111
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 182:5962-5968(2000).
-1- FUNCTION: STRUCTURAL COMPONENT OF THE DISTAL-HALF TAIL FIBER. IT CONSTITUTES THE PART OF THE LONG TAIL FIBERS THAT RECOGNIZES THE
                                                                                                            Nucleic Acids Res. 24:4420-4449(1996).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: TO THE C-TERMINAL SECTION OF M.PNEUMONIAE MPN308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JN-2002 (Rel. 41, Created)
JN-2002 (Rel. 41, Last sequence update)
NN-2002 (Rel. 44, Last annotation update)
tail fiber protein p37 (Protein Gp37) (Receptor recognizing
                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                  Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                   Score 78; DB 1; Length 264;
Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                               Hypothetical protein; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
84F1B7716ACB928F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 MMLAGVVTMAVTRLTEIVLPF-----TFANNYNRKLKNSLNIAL 150
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                               SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                   EMBL; AE000007; AAB95706.1; -.
                                                                                                                                                                                                                                                                                                                                  235 P
28961 MW;
                                                                                                                                                                                                                                                                                                                                                                   8.6%;
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                 115
166
201
                                                                                                                                                                                                                                                                                                                                             264 AA;
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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          NCBI_TaxID-2104;
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15-JUN-2002
15-JUN-2002
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Q9G0B5;
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                                                                                                     pneumoniae.
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TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                   CENTER KINK OF THE FIBER AND THE CARBOXYL END AT THE DISTAL TIP. THE OTHER POLYPEPTIDES ARE DISTRIBUTED UNIFORMLY ALONG THE LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 FSVNNGTKTFLFSPSETTSLRKFVAGYSTNGTDLTTPPTENYALATVVTYHDNNAFGDGQ 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 FAQGDILGGSLILGFDAVGI-----GLILTGAYLDI------KDFDNNAKKADFKW-T 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 TLLGYYQGGNYHHYFRGKGTTNINTHGGLLVTPGIIDVIGGSVNIDGRNNASTAMFKGNT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WGKGMMLAGVVTMAVTRLTEIVLPFTFANNYNRKLKNSLNIA--------- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 TG-----SSSVDNMTISVWGNTFTNPSEGNRKNVMEISDATSWMSYIQRLTTGEVE 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77; Gaps
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LENGTH OF THE DISTAL HALF-FIBER, WITH THE AMINO END NEAR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75;
                                                                                                                                                  SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF208841; AAG29754.1; -.
                                                                                                                  THE DISTAL HALF-FIBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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March 14, 2003, 14:22:51; Search time 24.1966 Seconds (without alignments) 1507.249 Million cell updates/sec
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908
1 MNKFLIFILVIFCAFSSFAQ......DINMGQASALGFGLSFKKSY 177
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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671580 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries inimum DB seq length: 0 Maximum DB seq length: 2000000000

SPTREMBL_21:*

sp_organelle:*
sp_phage:*
sp_phant:*
sp_rodent:*
sp_vrus:*
sp_vartebrate:*
sp_vartebrate:*
sp_vartebrate:* 1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_manmal:*
7: sp_mhc:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* 1101 1121 1131 1151 1161 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	09x3v0 borrelia ga	Q9x3u9 borrelia af	O51065 borrelia bu	O50896 borrelia bu	O50885 borrelia bu	Q9s011 borrella bu	O50696 borrelia bu	031325 borrelia bu	Q9kxk6 streptomyce	Q92fbl listeria in	Q91hx2 oryza sativ	Q93re6 vibrio para	Q92wnl rhizobium m	Q22972 caenorhabdi	Q8vs09 klebsiella	Q8rfal fusobacteri
QI QI	09x3V0	99x3U9	051065	050896	050885	Q9S011	969050	031325	09 KXK6	Q92FB1	Q9LHX2	Q93RE6	Q92WN1	022972	08VS09	Q8RFA1
DB	7	7	16	16	16	7	16	7	16	16	10	7	16	2	7	16
% Query Match Length DB	177	178	179	161	170	161	190	95	289	779	375	427	376	389	427	447
% Ouery Match	100.0	9.98	81.2	34.0	33.2	26.7	26.4	18.8	10.5	10.2	10.0	10.0	9.7	9.5	9.5	9.5
Score	908	786.5	737	309	301.5	242.5	240	170.5	95.5	93	91	90.5	88.5	86.5	86.5	86.5
Result No.	-	7	m	4	ഗ	9	7	80	σ	10	11	12	13	14	15	16

Q9uy78 pyrococcus Q8xd36 escherichia Q913r9 helicobacte Q9xd03 desulfitoba Q8z19 salmonella Q8z19 salmonella Q8z19 salmonella Q8z18 salmonella Q8z18 salmonella Q8z18 salmonella Q8z18 salmonella Q9z18 salmonella Q9x18 lactobacte Q68x12 necator ame Q305x10 helicobacte Q8r9D2 fusobacterila Q2009 helicobacterila Q2011 necator ame Q31x1 nanabaena sp Q8x121 nanabaena sp Q9x16 thermotoga Q51x1 nanabaena sp Q9x16 thermotoga Q51x1 lanabaena sp Q9x16 thermotoga Q51x1 lanabaena sp Q9x16 thermotoga Q51x1 lanabaena sp Q9x16 thermotoga Q51x1 lorrella bu Q9x17 clostridium Q93x17 clostridium Q8y17 clostridium	Q9f0jl s Q8rew2 Q92iv6
17 Q9UY78 16 Q8XD36 2 Q9L3R9 16 Q8XLU8 16 Q8XLU8 16 Q8XLU8 16 Q8XR98 16 Q8XR98 16 Q8XR12 2 Q9ANV6 16 Q8XR12 2 Q30550 16 Q8KR12 16 Q8KCB2 16 Q8KCB2 16 Q8KCB2 16 Q9KCB2 16 Q9XLG 16 Q9XLG 16 Q9XLG 16 Q9XRG 16 Q97RG 16 Q97RG 16 Q97RG 16 Q97RG 16 Q97RG 16 Q97RG 16 Q97RG 17 Q97RG 18 Q97RG 19 Q97RG 11 Q97RG 11 Q97RG 11 Q97RG 12 Q97RG 13 Q97RG 14 Q97RG 16 Q97RG 17 Q97RG 18 Q97RG 19 Q97RG 10 Q97RG 11 Q97RG 11 Q97RG 12 Q97RG 13 Q97RG 14 Q97RG 15 Q97RG 16 Q97RG 17 Q97RG 18 Q97RG 19 Q97RG 10 Q97RG 11 Q97RG 11 Q97RG 12 Q97RG 12 Q97RG 13 Q97RG 14 Q97RG 15 Q97RG 16 Q97RG 17 Q97RG 18 Q97RG 18 Q97RG 18 Q97RG 18 Q97RG 19 Q97RG 10 Q97RG 10 Q97RG 11 Q97RG 11 Q97RG 12 Q97RG 12 Q97RG 13 Q97RG 14 Q97RG 15 Q97RG 16 Q97RG 17 Q97RG 18	2 Q9F0J1 16 Q8REW2 16 Q92IV6
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STRAIN=ATCC 35210 / B31;

STRAIN=B8065943; PubMed=9403685;

REDLINE=89065943; PubMed=9403685;

Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmar W.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                          60 GSFAQGDILGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKADFKWTWGKGMMLAGVVT 119
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
Noppa L., Ostberg Y., Bergstrom S.;
"Pl3, a novel integral membrane protein of Lyme disease Borrelia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       MAVTRLTEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177
                                                                                                                                                                                                Noppa L., Ostberg Y., Lavrinovicha M., Bergstrom S.; "Pl3, an integral membrane protein of Borrelia burgdorferi, is C-terminally processed and contains surface-exposed domains."; Infect. Immun. 09:3323-3334(2001).
EMBL; AF085740; AAD28361.1; -SEQUENCE 178 AA; 19194 MW; C1C032EB55320C86 CRC64;
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                                                                                                                                                                                                                                                                                  Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                          Indels
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                Spirochaetales; Spirochaetaceae; Borrelia
                                                                   Last sequence update)
Last annotation update)
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1-JUNR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein BB0034.
BB0034 OR P13.
                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                 Score 786.5; DB 2 Pred. No. 1.1e-62;
                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                         Created)
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                                  PRT;
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                                                                                                                                                                                                                                                                                86.6%;
                                                      01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                        Matches 154; Conservative
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                                PRELIMINARY;
                                                                                           Membrane protein P13
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                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID=29518;
                                                                                                                  Borrelia afzelii.
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                                                                                                                                Bacteria;
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SEQUENCE FROM N.A.
STRANN=ATCC 35210 / B31;
STRANN=ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocaphe J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                      61 SFAQGDILGGSLILGFDAVGIGLILFGAYLDIKDFDNNAKKADFKWTWGKGMMLAGV-VT 119
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                                                                                                                                                                                                                                                                                                                  119 TMAVTRLTEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177
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                                                                                                                                                                                  81.2%; Score 737; DB 16; Length 179;
81.0%; Pred. No. 3e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AE001117; AAC66426.1; --
EMBL; AF085739; AAD28360.1; -.
                                                              EMBL, .....TIGN: BB0034; -.
TIGN: BB0034; -.
Hypothetical protein; Complete proteome.
GROUTENCE 179 AA; 19104 MW; FD6056E8E24E5D5D CRC64;
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161 AA; 17887 MW; D93BDB326FE2DA30 CRC64;
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NCBL_TaxID=139;
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Last annotation update)
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EMBL; AE000790; AAC66226.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20,
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Matches 74; Conserv
                                                                                                                                                                                                            Best Local Similarity
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us-09-508-487-23.rspt

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EMBL; AE001584; AAF07707.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 161 AA; 17016 MW; 14D4906CC8107CD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   burgdorferi.
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SERAINA-ATCS 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathjgra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlawage A.R., Quackenbush J., Salzberg S., Hanson M.,
Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Ulterback T., Watthey L., McDonald L., Artlach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Lathigra R., White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-Vugt R., Palmer N., Haft D., Rosa P., Stevenson B.;
"A bacterial genome in flux: The twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease splrochete Borrelia burgdorferi.";
Mol. Microbiol. 00-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SFAQGDILGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKADFKWTWGKGMMLAGVVTM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 SFVQGDYIGGGAVLGSQLLGGILCIAGNILGHTDDETRA-----TTGHIITTIGVGTI 118
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119 IASHIASLIIPFTFANKHNANLKKRLGIDIAGFEPNFDIGIS-----GFQLSFKKRY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AVTRLTEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.2%; Score 301.5; DB 16; Length 140.1%; Pred. No. 2.2e-19;
tive 23; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                           "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                      710K; BB131; -
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 170 AA; 18227 MW; 0E71B633EA80FB22 CRC64;
                                                                                                                                                 Plasmid 1p28-4.
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid 1p56.
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                    Borrelia burgdorferi (Lyme disease spirochete).
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                                          170 AA
                                                                    Created)
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                     burgdorferi.";
Nature 390:880-586(1997).
EMBL; AE000789; AAC66194.1; --
TIGR; BBI31; --
                                                                 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20, Hypothetical protein BBI31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 40.19
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                                         PRELIMINARY;
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                                                                                                                                                                           NCBI_TaxID=139;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlawage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weldman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                        95 FDNNAKKADFKWTWGKGMMLAGVVTMAVTRLTEIVLPFTFANNYNRKLKNSLNIALGGFE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 FDAVGIGLILTGAYL--DIKDFDNNAKKADFKWTWGKGMMLAGV--VTMAVTRLFEIVLP 131
                                                         Gaps
                                                                                                             18 FAQDDSKSTFNLGAGE--KFLVYETNKKDSLVPFLLNLFLGFGIGSFAQGDILGGSLILG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 LVYETNKK-DSLVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILTGAYLDIKD 94
                                                                                                                                             4 FAQEKLEK----GVGDIATVMKYESKKATILAPLLLNIFLSLGIGSFVQGDYIGGGALLG
                                                      17;
Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 26.4%; Score 240; DB 16; Length 190; I Similarity 41.3%; Pred. No. 7.9e-14; 59; Conservative 22; Mismatches 50; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 190 AA; 21813 MW; A80FBBBCAD4B13EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
26.7%; Score 242.5; DB 2; 39.3%; Pred. No. 3.9e-14; iive 25; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 AA.
                                                                                                                                                                                                                                                                                                                                                                   132 FTFANNYNRKLKNSLNIALGGFEPSFDINM 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSFDINMGQASALGFGLSFKKSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390:580-586(1997).
EMBL; AE000784; AAC65989.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein BBH41.
BBH41.
                                                      59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid lp28-3
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128 IVLPFTFANNYNRKLKNSLNIA---LGGFEPSFDI-
                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lij
SEQUENCE FROM N.A.
STROVAR 6A;
                                                                                                                                                                                                                                                                                                                                            Hypothetical protein lin0195.
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                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                            Listeriaceae; Listeria.
NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ListiList; LIN00195; ~.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      Listeria innocua.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=11679669;
                                                                                                                               116 IGAGM 120
                                                                                     167 LGFGL 171
                                                                                                                                                                                                                                                                               01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                        01-MAR-2002
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                                                                                                                                                                                                                                       Q92FB1
                                                                                                                                                                                             RESULT 10
Q92FB1
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Q9LHX2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 SLILGFDAVGIG---LILTGAYLDIKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRLTE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SERGIN-A3(2), M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             18.8%; Score 170.5; DB 2; Length 95; 45.0%; Pred. No. 5.6e-08; tive 11; Mismatches 32; Indels ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 289;
                                                                                                                                                                                                                                                                                                                        on the Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL357591; CAB93434.1; -.
SEQUENCE 289 AA; 29123 MW; 89AD68D9D805BE10 CRC64;
                                                                                                                                                                                                                                                                                              Feng S., Das S., Barthold S.W., Fikrig E.;
"Characterization of two genes, pl1 and p5, on the Bon burgdorferi 49-K110 base linear plasmid.";
Blochim. Blophys. Acta 1307:270-272(1996).
EMBL: L41111, AABC2881.1;
SEQUENCE 95 AA: 10739 MW; D12F6791F8920C3A CRC64;
                                                                                                                                                                     Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 43;
                                                                                                                                                 Borrelia burgdorferi (Lyme disease spirochete)
  95 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 AA.
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                                            Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative integral membrane protein. SCO2314 OR SCC53.05.
                                                                                                                                                                                                                                                      STRAIN=N40;
MEDLINE=96305348; Pubmed=8688460;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFVQGDYIGGGSVLGFNLLG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFAQGDILGGSLILGFDAVG 80
                 031325;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coelicolor A3(2).";
Nature 417:141-147(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                       (clone 8) s3.
S3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9KXK6
Q9KXK6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Britan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
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Jones L.-M., Kaerst U., Kreft J., Kunb M., Kunst F., Kurapkat G.,
A Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,
A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
A Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.",
Eschence 224:849-852(2001).

EMBL, AL596163; CAC95428:1; -.
                                                                      64 VVV-----NRAMPOPKKVAGLDLGOFGIAFTVFAAWCALGNIFDPAGAFDNDGGASG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 19, Last annotation update)
Similar to Arabidopsis thaliana chromosome II sequence from clones T22013 (OSJNBa0038J17.30 protein).
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 TMAVTRLTE-----IVLPFTFAN------NYNRKLKNSLNI 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein, Complete proteome.
SEQUENCE 779 AA; 89623 MW; AB7B7D066C715261 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.2%; Score 93; DB 16; 26.6%; Pred. No. 5.7; iive 24; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                         779 AA.
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90 LDIKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRLTEIVLPFTFANNYNRKLKNSLNIA 149
                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative sugar ABC transporter permease protein.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RB0301 OR SMB20315.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                      376 AA.
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26.1%; Pred. No. 6;
tive 19; Mismatches
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                                                                                                                                                            231 GGLF--AYHAIMGQAGVQG 247
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les 49; Conserv
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Q92WN1
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Q22972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio parahaemolyticus.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 ---PFLLNLFLGFGIGS--FAQGDILGGSLILGFDAVG-----IGLILTGA-----Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 GMMLAGVVTMAVTRLTEIVLPFTFANNYNRKLKNSLNIALG------GFEPS 156
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC clone:OSJNBa0038J17.";
                                                                                                                                          Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic, DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 427;
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A Akeda Y., Honda T.;
T. "Vibrio parahaemolyticus adhesin gene.";
T. "Vibrio parahaemolyticus adhesin gene.";
Submitted (Aug-2000) to the EMBL/GenBank/DDBJ databases.
SR EMBL, AB047560; BAB59008.1;
DR InterPro; IPR002528; MatE.
DR Pfam; PF01554; UPF0013; 2.
DR Pfam; PF01554; UPF0013; 2.
DR TIGRPAM; TIGRON970; MATE:; 1.
TIGRPAM; TIGRON970; MATE:; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.0%; Score 91; DB 10; Length 375; 24.3%; Pred. No. 3.6;
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                                                                                                                                                                                                                                        Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001633; BAA94232.1; -.
EMBL; AP003104; BAB55738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001087; Lipase_GDSL.
SEQUENCE 375 AA; 40234 MW; 238D34ACAD934E93 CRC64;
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Last annotation update)
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26.1%; Pred. No. 4.6;
tive 23; Mismatches
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Ehrhartoideae; Oryzeae; Oryza NCBI_TaxID=4530;
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Matches 42; Conservative
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hes 52; Conservative
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                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
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10; LWL-----KKHIIAFGWGD--IRASLVLDKITRFLSLSLPTTF-----NFLAWA 230 Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.;
"The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-NVLVVALAVVF-------AGETFLSLYNFQSMSAQVPELALLALGVMLA 106 61 SFAQGDILGGSLILGFDAVGIGLIL---TGAYLDIKDFDNNAKKAD--FKWTWGKGMMLA 115 GV-----VTMAVTRLTEIVLPF---TFANNYNRKLKNSLNIALGGFEPSFDINMGQAS 165 Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID=6239; 2 NKFLIFILVIFCAFSSFAQDDSKSTFNLGAGEKFL-VYETNKKDSLVPFLLNLFLGFGIG Plasmid pSymB (megaplasmid 2).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium. 45; Length 376; Indels fixing endosymbiont Sinorhizoblum meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
EMBL; AL603643; CAC48701.1; -.
InterPro; IPR001851; Bac_innem_transp.
Plassmid; Hypothetical protein; Complete proteome.
SEQUENCE 376 AA; 39929 MW; 7DB5E8189CFAF827 CRC64;

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Search completed: March 14, 2003, 14:27:07 Job time: 27.1966 secs
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Lengeler J.W.;

"The genes and enzymes for the catabolism of galactitol, D-tagatose, and related carbohydrates in Klebsiella oxytoca M5al and other enteric bacteria reflect a modular evolution.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF416702; AAL60172.1;

InterPro; IPR004703; Gal_spec_IIC.

InterPro; IPR001865; Ribosomal_S2.
                                                                                          Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Gardner A., Green P., Hawkins T., Hallier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P.,
Barsons J., Percy C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Willkinson-Spreat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: 04(4851; AAC47989.1; -. HSSP: P00797; 2REN.
InterPro; IPR001461; AspproteaseA1.
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PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.
SEQUENCE 389 AA; 42238 MW; A76270702C900C98 CRC64;
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Last annotation update)
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-94150718; Pubmed-7906398;
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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SEQUENCE FROM N.A.
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NCBI_TaxID=571;
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DFDNNAKKADFKW-----TWGKGMMLAGV-----VTMAVTRLTEIV-----LP 131
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                                                                                                                                                                39; Indels
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TIGRPMs; TIGR00827; EIIC-GAT; 1.
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SEQUENCE 427 AA; 45406 WW; 1D1817F0287F7F56 CRC64;
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Best Local Similarity 25.4%; Pred. No. 11;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2003, 14:23:06; Search time 10.9382 Seconds Run on:

(without alignments)
476.116 Million cell updates/sec

US-09-508-487-23 908 1 MNKFLIFILVIFCAFSSFAQ......DINMGQASALGFGLSFKKSY 177 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

Ainimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			COLUMNICO		
Result		Query					
No.	Score	Match	Length DB	DB	ID	Description	
Н	87	9.6	828	4	US-09-255-829-22	Sequence 22, Appl	
2	87	9.6	828	4	US-09-255-829-29	29.	
m	87	9.6	1169	4	US-09-255-829-20	20,	
4	77		243	4	US-09-134-001C-2961	2961	
2	74.5	8.2	934	4	US-08-840-466A-19	Т	
9	74.5	٠	934	4	US-09-696-188B-19	19,	
7	71		612	m	US-09-295-186-16	16,	
æ	70.5		95	4	US-08-851-362D-37	37,	
g	70.5	7.8	116	4	US-08-851-362D-49	49	
10	70.5	•	344	4	US-09-134-001C-4175	4175	
11	70.5		581	4	US-09-393-627B-1	ı,	
12	69		376	Н	US-08-608-241-2	7	
13	69		376	7	US-08-922-182-2	Sequence 2, Appli	
14	69	٠	376	7	US-08-919-953-2	7	
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16	69	7.6	415	4	US-09-134-001C-5101	510	
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18	99	•	539	7	-80		
19	89	7.5	539	~	US-08-838-189D-2	7	
20	68	•	539	m	08-852-	2,	
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22	89	7.5	539	4	US-08-467-969A-2	7	
23	68	7.5	539	4	08-467	7	
24	68	7.5	539	4	US-08-001-554A-2	7	
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56	67.5	7.4	349	4	US-09-134-001C-4004		
27	67.5	7.4	538	4	US-09-134-001C-4633	Sequence 4633, Ap	

7;

Gaps

40;

Query Match 9.6%; Score 87; DB 4; Length 858; Best Local Similarity 22.8%; Pred. No. 0.22; Matches 38; Conservative 31; Mismatches 58; Indels

4 (1 (1 0) 11 0) 11 0) 11 0)	Sequence 12, Appli Sequence 12, Appl Sequence 5, Appli Sequence 5196, Ap Sequence 10, Appl Sequence 5661, Appl
US-08-790-912-4 US-08-933-750C-22 US-09-234-613-22 US-08-312-387B-5 US-08-683-426-5 US-08-683-426-12 US-08-683-458-5 US-08-683-458-5 US-08-683-458-5 US-08-683-458-5 US-08-683-458-5 US-08-681-360-5 US-08-78-78-1408-5	US-09-333-412-5 US-09-333-412-12 US-09-338-943-5 US-09-134-001C-5196 US-09-134-001C-5661
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#### ALIGNMENTS

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OPERATURE SYSTEM: PC-LOUS/MS-LOUS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CB97/02273
FILING DATE: 22-30G-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT WREGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REJECOMMUNICATION INFORMATION:
MARKE: PLOUS NUMBER: 1581.0130002
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Oulnn, Conrad Padraig
APPLICANT: Oulnn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                           Sequence 22, Application US/09255829 Patent No. 6461617\,
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TELEFAX: 202-371-2540
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MOLECULE TYPE: protein
US-09-255-829-22
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                      80 GIGLILTGAYLD-----IKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRL------ 125
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                                                                                                                                                                                                   722 ALNYQAQALEEIIKYRY-NIYSEKEKSNINIDFNDINSKLNEGINQA 767
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                                                                                                                                                                        -----TEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATE: US/09/255,829
FILING DATE: 23-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Reith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.6%; Score 87; DB
ilarity 22.8%; Pred. No. 0.22
Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0130002
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 23-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-ANG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      Sequence 29, Application US/09255829; Patent No. 6461617; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
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MOLECULE TYPE: protein
US-09-255-829-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WASHINGTON
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Best Local Similarity
Matches 38; Conserv
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37 VYETNKKDS-
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              662 VVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYK 721
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                                                                                                                                                                                                                                                                                                                         3: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C. 1100 NEW YORK AVENUE, NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                         Sequence 20, Application US/09255829
Patent No. 6461617
GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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FILING DATE: 22-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 23-FEB-199
PRIOR APPLICATION DATA:
APPLICATION APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                        COURINI. ZOOD5-3934
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: ESMOND, ROBERT W. REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                        US-09-255-829-20
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STATE:
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Matches
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Score 74.5; DB 4;
Pred. No. 6.7;
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-09-696-1888-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/840,466 FILING DATE: 1997-04-18 ATTORNEY/AGENT INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-08-840-466A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/09696188B Patent No. 6406885 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
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21.78;
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                Conservative
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Best Local Similarity
                                                                                          Similarity
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                                                                                                              34;
                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TGFLTIFVLAG----LLIGGLGSALTGIFPILSLVMGILIALLGLGMLFGK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                16 GIMSFSFLFILTAGMVAAFNPCGIALLPSYISYL---IGGETKDHSFRYAIFKGLGLGG 71
            EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garrett
                                                                                                                                                                                                                                                                                                                         DB 4; Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Boone, Laural S.
REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 04995.0029-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow,
                                                                                                                                                                                                                                                                                                                                                                  54;
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STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/840,466A FILING DATE: 18-Apr-1997 CLASSIFICATION: <un>
    FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2961
                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
                                                                                                                                                                                                                                                                                                                         Score 77;
Pred. No.
                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-840-466A-19; Sequence 19, Application US/08840466A; Patent No. 6261561; GENERAL INFORMATION:
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O'Brien, Alison D.
Wachtel, Marian R.
TITLE OF INVENTION: Method Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                         8.5%;
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MOLECULE TYPE: peptide
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STATE: D.C.
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APPLICANT: Stewart, C. Neal
McKee, Marian L.
O'Brien, Alian D.
Wachtel, Marian R.
Wachtel, Marian R.
TITLE OF INVENTION: Method Of Stimulating An Immune Response
By Administration Of Host Organisms That Express Intimi
Alone Or As A Fusion Protein With One Or More Other 7; 82 GLILTGAYLDIKDFDNNAKKADFKW-TWGKGMMLAGVVTMAVTRLTEIVLPFTFANNYNR 140 ---HKKDYDE 324 DSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGI 81 252 DSRFTANLGAGORF-----FLPANMLGYNV--FIDQDFSGDNTRLG----Length 934; Garrett Indels SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/696,188B
FILING DATE: S-Oct-2000
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION DATA: NAME: Boone, Laural S.
REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 04995.0029-00000
TELECOMMUNICATION INFORMATION: ADDRESSEE: Finnegan, Henderson, Farabow, Dunner, L.L.P. STREET: 1300 I Street, N.W., Suite 700 .; ***** ---IGGEYW--RDYFKSSVNGYFRMRRWHESY-----325 RPANGFDIRFNGYLPSY-----PALGAKLIYEQYY 354 141 KLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177 DB 8.2%; Score 74.5; Di 21.7%; Pred. No. 6.7; :ive 22; Mismatches

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Query Match
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Matches 1
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                                                           82 GLILTGAYLDIKDFDNNAKKADFKW-TWGKGMMLAGVVTMAVTRLTEIVLPFTFANNYNR 140
                                                                                                                                                            -----HKKDYDE 324
    55; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LGGSLILGFDAVGIGLI-LTGAYLDIKDFDNNAKKADFKWT---- 107
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hasida, Miyoko
APPLICANT: Tsutsumi, No. 6127137iko
APPLICANT: Tsutsumi, No. 6127137iko
APPLICANT: Haliker, Torben
APPLICANT: Stringer, Mary Ann
TITLE OF INVENTION: Methods of Using Thereof (As Amended)
TITLE OF INVENTION: Methods of Using Thereof (As Amended)
TITLE REFERENCE: 4953.204-US
CURRENT APPLICANTON NUMBER: US/09/295,186B
CURRENT FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: PCT/DK97/00490
PRIOR APPLICATION NUMBER: PCT/DK97/00490
PRIOR APPLICATION NUMBER: PCT/DK97/00490
PRIOR APPLICATION NUMBER: 1997-10-31
SROFTWARE: FastSEQ.for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
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APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gala, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
TITLE OF INVENTION: Growth Factor Receptor
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362D
UNMBER OF SEQ 1D NOS: 49
    46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 612;
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                                                                                                                                                                                                                   141 KLKNSLNIALGGFEPSFDINMGQASALGFGLSFKKSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.8%; Score 71; DB 3 Best Local Similarity 26.4%; Pred. No. 9.4; Matches 33; Conservative 12; Mismatches
    Mismatches
                                                                                                                                         291 ---IGGEYW--RDYFKSSVNGYFRMRRWHESY----
                                                                                                                                                                                                                                                                                                            US-09-295-186-16
; Sequence 16, Application US/09295186B
; Patent No. 6127137
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22;
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Conservative
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34;
Matches
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: DEPLEMATIOS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4175
LENGTH: 344
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                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Grailo, Michael
APPLICANT: Grailo, Michael
APPLICANT: Grailo, Michael
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
TITLE OF INVENTION: Growth Factor Receptor
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362b
CURRENT FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 49
SOFTWARRE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                 7.8%; Score 70.5; DB 4; Length 95; 23.0%; Pred. No. 0.83; ive 13; Mismatches 27; Indels
  FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 49, Application US/08851362D Patent No. 6235883
                                                                                                                                                                                         23.0%;
                                                                                                                                                                                                                  17; Conservative
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                           153 FEPSFDINMGQASA 166
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                                                                                                                                                                                                                                                                                                                                                                                           53 SKTQFSLKLSSVTA
                                                                                                                                                                                            Similarity
                                                                       ; TYPE: PRT
; ORGANISM: human
US-08-851-362D-37
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ORGANISM: human
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US-08-851-362D-49
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SOFTWARE: Factor SEQ ID NO 37 LENGTH: 95
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97 NNAKKADFKWTWGK-------GMMLAGVVTMAVTRLTEI-VLPFTFANNYNRK 141
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                 APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
NUMBER OF SQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.6%; Score 69; DB 1
Best Local Similarity 25.3%; Pred. No. 8.2;
Matches 37; Conservative 23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9602:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08922182 Patent No. 5834300 GENERAL INFORMATION:
APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 376 amino acids amino acid
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                          COUNTRY:
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209 YIIIVLVIV-----YANFNANAVFNLLNIIGSMVIVVWGSSIWSQIRLRQAIKKQGKNPD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 LG----FDA------VGIG-LILTGAY-LDIK------DFDNNAKKADFKWTWGKGM 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 ML-AGVVTMAVTRLTEIVLPFTFANNYNRKLKNSLNIALG-GFEPSFDINMGQASALGFG 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                 45 SLVPF------LINLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILTGAY 89
                                                                                                                                                                 --GAGEKFLVYETNKK----D 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 DSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFGIGSFAQGDILGG-----SLI 73
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                                                                               DB 4; Length 344;
                                                                                                                      34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KOVESGI, INTERED.
APPLICANT: ROSEIVINK, PETTUS W.
APPLICANT: Bruder, Joseph T.
TITLE OF INVENTION: ALEFANATION TALEFANATION TALEFANATION TO THE TELEMER: 202345
CURRENT APPLICATION NUMBER: US/09/393,627B
CURRENT PILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/099,851
PRIOR APPLICATION NUMBER: US 60/136,529
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 3.2
SOFTWARE: PATENTIN VET. 2.2
                                                                             Query Match 7.8%; Score 70.5; D
Best Local Similarity 26.6%; Pred. No. 4.9;
Matches 33; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Human adenovirus serotype 5
            ORGANISM: Staphylococcus epidermidis US-09-134-001C-4175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09393627B
Patent No. 6455314
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Kovesdl, Imre
                                                                                                                                                             4 FLIFILVIFCAFSSFAODDSKSTFNL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-608-241-2
Sequence 2, Application US/08608241
Patent No. 5747328
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Donohue, Timothy J
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LSF 383
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IS-09-393-627B-1
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LENGTH: 581
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Indels

DB 1; Length 376;

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97 NNAKKADFKWTWGK--
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Best Local Similarity
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                                                                                                                                                                                                    linear
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Best Local Similarity
Matches 37; Conserv
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                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 NNAKK-----EWGERFGMTHFVNPSEIDGDVVAHLVNMTKTPFDQIGGADYTFDCTGNVK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFLLNLFLGFGIG-----SFAQGDILGGSLILGFDAVGI----GLILTGAYLDIKDFD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Withuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
CORRESPONDENCES: 7
ADDRESSEE: Quarles & Brady
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
7.6%; Score 69; DB 2
Best Local Similarity 25.3%; Pred. No. 8.2;
Matches 37; Conservative 23; Mismatches
                                                                                                                                                                                                              NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93511
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 -LKNSLNIALGGFEPSFDINMGQASA 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
FILING DATE:
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-919-953-2; Sequence 2, Application US/08919953; Patent No. 5837481
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     376 amino acids
                                                                                                                                                                                                                                                                                                                                                                   : amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-922-182-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09192983A
Fatent No. 642244
General INFORMATION:
APPLICANT: Bonohue, Timothy
APPLICANT: Barber, Robert
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: Remediation
TITLE OF INVENTION: Remediation
FILE REPERENCE: 960296.95505
CURRENT APPLICATION NUMBER: US/09/192,983A
CURRENT FILING DATE: 1998-11-16
EARLIER RILING DATE: 1998-11-16
EARLIER PELING DATE: 1997-08-29
EARLIER FILING DATE: 1997-08-29
EARLIER FILING DATE: 1997-08-29
MUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                       DB 2; Length 376;
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               27,386
mp· 960296.93511
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25.3%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.6%; Score 69; 25.3%; Pred. No. 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT (CRANISM: Rhodobacter sphaeroides US-09-192-983-2
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                         25.3%;
                                                                                                                                                                            376 amino acids
                                                                                                                                                                                                                                                                                                                                               37; Conservative
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                                                                                                       TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-919-953-2
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Search completed: March 14, 2003, 14:27:50 Job time : 13.9382 secs

us-09-508-487-23.rai

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March 14, 2003, 14:25:51 ; Search time 9.94382 Seconds
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820.439 Million cell updates/sec
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908
1 MNKFLIFILVIFCAFSSFAQ......DINMGQASALGFGLSFKKSY 177
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                      199416 seqs, 46092074 residues
                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                    Run on:
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Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100% inimum DB seq length: 0 Maximum DB seq length: 2000000000

Published_Applications_AA: Database :

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/cgn2_6/ptodata/2/pubpaa/US07_MRW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 422, App	Sequence 22, Appl	Sequence 25, Appl	Sequence 11462, A	Sequence 3927, Ap	Sequence 2, Appli	Sequence 6850, Ap	Sequence 19, Appl	Sequence 4686, Ap	Sequence 6813, Ap	Sequence 10, Appl	Sequence 10, Appl	Sequence 6860, Ap	Sequence 53, Appl	Sequence 20, Appl	Sequence 6, Appli	Sequence 8, Appli	Sequence 18, Appl	Sequence 20, Appl
ID	US-09-741-669-422	US-09-910-186A-22	US-10-011-588-25	US-09-815-242-11462	US-09-738-626-3927	US-09-948-777-2	US-09-738-626-6850	US-08-837-459-19	US-09-738-626-4686	US-09-738-626-6813	US-10-060-763-10	US-10-063-763-10	US-09-738-626-6860	US-09-187-693-53	US-09-767-041-20	US-09-870-203A-6	US-09-870-203A-8	US-09-870-203A-18	US-09-870-203A-20
DB	10	6	σ	10	δ	10	σ	œ	6	6	σ	12	σ	σ	10	10	10	10	10
Query Match Length DB	451	413	852	206	544	544	417	934	406	421	670	670	513	95	410	579	579	579	579
Query Match	9.7	9.6	9.6	9.0	8.6	8.6	8.4	8.2	8.0	8.0	7.9	7.9	7.9	7.8	7.8	7.8	7.8	7.8	7.8
Score	88.5	87	87	81.5	78	7.8	76.5	74.5	73	73	72	72	71.5	70.5	70.5	70.5	70.5	70.5	70.5
Result No.	٦	7	3	4	S	9	7	80	σ	10	11	12	13	14	15	. 16	17	18	19

Sequence 10, Appl Sequence 12, Appl Sequence 2, Appli Sequence 4, Appli Sequence 14, Appl Sequence 16, Appl Sequence 5, Appl Sequence 1018, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 356, Appl Sequence 317, Appl Sequence 317, Appl Sequence 317, Appl Sequence 317, Appl Sequence 317, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl	Sequence 21, Appl Sequence 22, Appl Sequence 102, App
US-09-870-203A-10 US-09-870-203A-12 US-09-870-203A-2 US-09-870-203A-4 US-09-870-203A-14 US-09-870-203A-14 US-09-871-212-5 US-09-811-212-5 US-09-815-242-13341 US-09-815-242-13341 US-09-815-242-1333 US-09-815-242-1333 US-09-815-243-18 US-09-816-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-106 US-09-817-752A-133 US-09-810-729-134	US-09-813-453A-21 ) US-09-840-787-22 ) US-09-800-729-102
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 DFDNNAKKADFKW-----TWGKGMMLAGV-----VTMAVTRLTEIV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                   APPLICANT: POLSATION RATIL.
APPLICANT: Oblsen, Kari L.
APPLICANT: Oblsen, Kari L.
APPLICANT: 2yskind, Judith W.
TITLE OF INVENTION Genes identified as required for TITLE OF INVENTION: proliferation of E. coli FILE REFERENCE: ELITRA.009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 1999-12-19
PRIOR PILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-910-186A-22
; Sequence 22, Application US/09910186A
; Publication No. US20030009025A1
; GENERAL INFORMATION:
; APPLICANT: U.S. Army Medical Research & Material Command
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.7%; Score 88.5; DB 10; Best Local Similarity 27.5%; Pred. No. 0.18; Matches 30; Conservative 15; Mismatches 33;
                     ; Sequence 422, Application US/09741669
; Patent No. US2002022718A1
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Escherichia coli
                                             Patent No. US2002002
GENERAL INFORMATION:
US-09-741-669-422
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-741-669-422
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9.6%; Sco. 22.8%; Pred. No. v.c. 31; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11462, Application US/09815242
Patent No. US20020061569A1
                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                    Best_Local Similarity 22.8%
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-815-242-11462
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LENGTH: 206
                   SEQ ID NO 25
LENGTH: 852
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Sequence 25, Application US/10011588
Sequence 25, Application US/10011588
Sequence 25, Application US/10011588
Sequence 25, Application
Sequence 25, Application
Sequence 25, Application
Sequence 25, Application
TUTLE OF UNFORMING MELON SECONDINANT LIGHT CHAINS OF BOTULINUM
TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM
TITLE OF INVENTION: RECARRICH AND CLINICAL THERAPY
STILE OF INVENTION: RESERVED AND CLINICAL THERAPY
CURRENT APPLICATION NUMBER: US/10/011,588
CURRENT PRILING DATE: 2002-03-29
PRIOR FILING DATE: 2001-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 VVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYK 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 GIGLILTGAYLD-----IKDFDNNAKKADFKWTWGKGMMLAGVVŢMAVTRL-----
TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
TITLE OF INVENTION: NEUROTOXIN
FILE REPERENCE: A33626 A 06752.0107
CURRENT PAPLICATION NUMBER: US/09/910,186A
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: PCT/US00/12890
PRIOR FILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1993-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.6%; Score 87; DB 9; Length 413; Best Local Similarity 22.8%; Pred. No. 0.24; Matches 38; Conservative 31; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 -----TEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 ALNYQAQALEEIIKYRY-NIYSEKEKSNINIDFNDINSKLNEGINQA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic Construct US-09-910-186A-22
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PRIOR FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: 60/246,744
PRIOR APPLICATION NUMBER: 60/311,966
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 22
LENGTH: 413
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60 GSFAQGDILGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKADFKWTWGKGMMLAGV-- 117 37 VYETNKKDS-----LVPFL---LNLFLGFGIGSFAQG-DILGGSLILGFD----AV 79 FEATURE: ; OTHER INFORMATION: Recombinant protein encoded by SEQ ID NO:24 US-10-011-588-25 Length 206; APPLICANT: BASELDECK, KODELL
APPLICANT: Chisch, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
ITLE OF INVENTION: Identification of Essential Genes in TILE OF INVENTION: Prokaryotes
FILE OF INVENTION: Prokaryotes
FILE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/291, 078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-27
PRIOR PELICATION NUMBER: 60/253, 625
PRIOR FILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/253, 625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/253, 639
PRIOR FILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/269, 308
PRIOR FILING DATE: 2000-12-26
PRIOR PELICATION NUMBER: 60/269, 308
PRIOR FILING DATE: 2000-12-26
PRIOR PELICATION NUMBER: 60/269, 308
PRIOR PELICATION NUMBER: 60/269, 308
PRIOR PELICATION NUMBER: 60/200-12-26 80 GIGLILTGAYLD----IKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRL--Score 87; DB 9; Length 852; Pred. No. 0.56; Indels 721 ALNYQAQALEEIIKYRY-NIYSEKEKSNINIDFNDINSKLNEGINQA 766 126 -----TEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDINMGQA 164 Ouery Match 9.0%; Score 81.5; DB 10; Best Local Similarity 23.6%; Pred. No. 0.38; Matches 33; Conservative 21; Mismatches 37;

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FILE REFERENCE: 249-125
CURRENT APPLICATION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 6850
PRIOR APPLICATION NUMBER: DE 100 44 707.4
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6850
                                                                                                                                                                                     ; ORGANISM: Corynebacterium glutamicum US-09-948-777-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6850, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HAYASHI, MIKIRO
APPLICANT: CCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                               Query Match 8.69
Best Local Similarity 21.09
Matches 33; Conservative
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Matches 44; Conservative
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APPLICANT:
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                           103 DFKW------TWGK------TWGK------GMMLAGVVTMAVTRLTEI---- 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Patent No. US30020055115a1

Patent No. US30020055115a1

Patent No. US30020055115a1

APPLICANT: HUTHMACHER, Klaus

APPLICANT: PERFERLE, Malter

APPLICANT: BEFFERLE, Malter

APPLICANT: BATHE, Brigitte

APPLICANT: BATHE, Brigitte

TITLE OF INVENTION: NUCLECTIDE SEQUENCES CODING FOR THE DEP33 PROTEIN

FILE REFERENCE: 212556050X

CURRENT APPLICATION NUMBER: US/09/948,777

CURRENT FILING DATE: 2001-09-10
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    -----VTMAVTRLTE----IVLPFTFANNYNR--KLKNSLNIALG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 -VLPFTFANNYNRKLKNSLNIALG-----GFEPSF 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.6%; Score 78; DB (21.0%; Pred. No. 2.8; tive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TANGLI, NACKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                          ; Sequence 3927, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Corynebacterium glutamicum US-09-738-626-3927
                                                                                 --GFEPSFDINMGQASALGF 169
                                                                                                          187 TKGFEKNFSWNEADALTLGY 206
                                                                                                                                                                                                                                                                                  APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
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Best Local Similarity 21.0%
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                                                                                                                                                                                                       US-09-738-626-3927
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LENGTH: 544
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US-09-948-777-2
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                             103 DFKW-----TWGK------TWGK--------GMMLAGVVTMAVTRLTEI---- 128
                                                                                                                                                                                                                                         227 KFRWDYLGTFFMIVAATSLILFTTWGGSQYEWSDPIIIGLIITTIVAAALLVVVELRAKD 286
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                                                 99
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    Length 544;
                                              35; Indels
8.6%; Score 78; DB 10;
21.0%; Pred. No. 2.8;
tive 23; Mismatches 35
                                                                                                                                                                                                                                                                                           129 -VLPFTFANNYNRKLKNSLNIALG-----GFEPSF 157
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165 S-ALGFG 170
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US-09-738-626-4686
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US-09-738-626-6813
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APPLICANT:
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                                                                                                                                                                                                                                                                                     APPLICANT: McKee, Marian L.
APPLICANT: WcKee, Marian L.
APPLICANT: O'Brien, Alison D.
APPLICANT: Wachtel, Marian B.
TITLE OF INVENTION: Histidine-Tagged Intimin And Methods Of
TITLE OF INVENTION: Using Intimin To Stimulate An Immune Response And AS AN
TITLE OF INVENTION: Antigen Carrier With Targeting Capability.
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 LGTSSSAATIPVT----YQQTLKNDVDVNVAGFVVPLCATIHLAGSMMKIGLFTFAVVFM 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 GLILTGAYLDIKDFDNNAKKADFKW-TWGKGMMLAGVVTMAVTRLTEIVLPFTFANNYNR 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.2%; Score 74.5; DB 8; Length 934;
21.7%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner, L.L.P. STREET: 1300 I Street, N.W., Suite 700 STRET Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,459 FILING DATE: 18-APR-1997 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 RPANGFDIRFNGYLPSY-----PALGAKLIYEQYY 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: FORIS, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 04995.0023-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.7%; Pred. ...
+1ve 22; Mismatches
                121 AVTRLTEIVLPFTFANNYNRKLKNSLNIALGGFEP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         RESULT 8
US-08-837-459-19
'Sequence 19, Application US/08837459
'Patent No. US20020006407A1
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEO ID NO: 19
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  934 amino acids
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Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                   : | : : | :: | 304 YDMEVGVGLSIGF 316
                                                                                            157 FDINMGQASALGF 169
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TOPOLOGY: linear
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20005-3315
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RESULT 9

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57 ------FGIGSFAQGDILGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKADFK 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 IFILVIFCAFS-----SFAQDDSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLFLG-- 56
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                                                                                                                                                                                APPLICANT: OCHIALI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OCAKI, AKI
APPLICANT: OCAKI, AKI
APPLICANT: OCAKI, AKI
TILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-4-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 99/377484
Sequence 4686, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Corynebacterium glutamicum
US-09-738-626-4686
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Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                        MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIZOGUCHI, HIROSHI
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                               APPLICANT: NAKAGAWA, SATOSHI
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                                                                                                                                                          HAYASHI, MIKIRO
OCHIAI, KEIKO
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Best Local Similarity 24.6%
Matches 46; Conservative
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APPLICANT: CURLE, ROTY A.J.

TITLE OF INVENTION: No. US20010001663Alel Transporter-Like Genes and Uses Therefo
FILE REFERENCE: 10147-8
CURRENT APPLICATION NUMBER: US/10/063,763
CURRENT PILING DATE: 2002-01-30
PRIOR PILING DATE: 1999-JUL-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTING VET: 2.0
SEQ ID NO 10
LENGTH: 670
TYPE: PAT
ORGANISM: HOMO sapiens
US-10-063-763-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFAQGDILGGSLILGFDA-----VGIGLILTGAYLDIKDFDN-NAKKADFKWTWGKGM 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 MLAGVVTMAVTRLTEIVLPFTFANNYNRKLKNSL-----NIALGGFEPSFDINMGQAS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 NLSSNSFLCMENGTQILRPTQDPSECTKEVKSLMWYYVLVGNIVRG------MGETP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNKFLIFILVIFCAFSSFAQDDSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLFLGFGIG 60
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7.9%; Score 71.5; DB 9;
Best Local Similarity 18.6%; Pred. No. 13;
Matches 39; Conservative 28; Mismatches 68;
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15;
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR RILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
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APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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Publication No. US20020197605A1
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US-09-738-626-6860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: NAKACAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6860
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US-10-660-763-10
Sequence 10, Application US/10060763
Sequence 10, Deplication US/20060763
Publication No. US20030022286A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20030022286A1e1 Transporter-Like Genes and Uses Therefor CURRENT APPLICATION NUMBER: US/10/060,763
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----NEDYMWMNGVEMNYGRAITQDDVAAQRPVAVIAPDTF----NTLFDANPN 182
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                                                                                                                                                                                                                                                                                                                                                                   41 NKKDSLVP-----FLLNLFLG--FGI---GSFAQGDILGGSLILGFDAVGIGLILTGAYL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                   Length 421;
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                                                                                                                                                                                                                                                                                                                             47; Indels
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6.9;
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Pred. No. 15;
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21.9%; Pred. No. 15,
''ve 34; Mismatches
                                                                                                                                                                                                                                                                             8.0%; Score 73; DB 925.7%; Pred. No. 6.9; tive 19; Mismatches
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PELING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 6813
                                                                                                                                                                                                                 ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6813
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183 LALGS-EVAFELN-GQETFL 200
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Matches 36; Conservative
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; ORGANISM: Homo sapiens
US-10-060-763-10
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Best Local Similarity
Matches 42; Conserva
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US-10-063-763-10
                                                                                                                                                                                                  TYPE: PRT
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us-09-508-487-23.rapb

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Sequence 20, Application US/09767041

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANY: Smith, Hilda
APPLICANY: Smith, Hilda
APPLICANY: Smith, Hilda
APPLICANY: Smith, Hilda
APPLICANY: STREPTCOCCCUS SUIS VACCINES AND DIAGNOSTIC TESTS
FILE REFERENCE: 2183-4726
CURRENT APPLICATION NUMBER: DS/09/767,041
PRIOR APPLICATION NUMBER: PCT/NL99/00460
PRIOR APPLICATION NUMBER: EP98202465.5
PRIOR APPLICATION NUMBER: EP98202467.1
PRIOR APPLICATION NUMBER: 1998-07-22
PRIOR FILING DATE: 1998-07-22
                                                                                                -----IKDFDNNAKKADFKWTWGKGMMLAGVVTMAVTRLTEIV 129
                                                                                                                                           66 EPLGAMIMGATGMRGVVPTNEAIAGIAQAEYGAQVAWL----MILGFAISLVLARFTNLR 121
                                                                                                                                                                                                                                        122 YVFLTGHHVLFMSTMLTIILATAGFDAWIVVGVGALLLGILMVSLPAFAHPWTRRITGDD 181
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                           27; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 FLVYETNKKDSLVPFLLNLFLGFGIGSFAQ--GDILGGSL--ILGFDAVGIGLILTGAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 53, Application US/09187693

Patent No. US20020175629A1

GENERAL INFORMATION:

APPLICANT: JANDOVILE, Aya

APPLICANT: JANDOVILE, Aya

APPLICANT: Gallo, Michael

APPLICANT: Gallo, Michael

TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal

TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal

TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal

TITLE OF INVENTION: Human Monoclonal Antibodies

FILE REFERENCE: Cell 4.20 CIP2

CURRENT APPLICATION NUMBER: US/09/187,693

CURRENT FILING DATE: 1998-11-05

PRIOR FILING DATE: 1998-09-29

PRIOR FILING DATE: 1997-05-05

NUMBER OF SEQ ID NOS: 75

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 53

LENGTH: 95
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7.8%; Score 70.5; DB 9;
Best Local Similarity 23.0%; Pred. No. 2.1;
Matches 17; Conservative 13; Mismatches 27;
                                                                                                                                                                                           130 LPF--------
                                                                                                                                                                                                                                                                                           147 NIALGGFEPSFDINMGQASALGFGLSFKKS 176
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US-09-187-693-53
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US-09-767-041-20
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S-09-187-693-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 GFGIGSFAQGD------ILG--GSLIL------GF-DAVGIGLILTGAYLDI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 KDFDNNAKKADFKWTWGKG----MMLAGVVTMAVTRLTEIVLPFTFANNYNRKLKNSLN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 R----ILKTDNIKTIGKSVFIIVVLSATVENYIVNLSFVFMPICFC-----LLNSIS 398
                                                                                                                                                                                                                                                                                                                                                        59;
                                                                                                                                                                                                                                                                                                     DB 10; Length 410;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                             5 LIFILVIFCAFSSFAQDDSKSTFNLGAGEKFLVYETNKKDSLVPFLLNLF-
                                                                                                                                                                                                                                                                                            Query Match 7.8%; Score 70.5; DB 10; Best Local Similarity 23.5%; Pred. No. 12; Matches 42; Conservative 26; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: March 14, 2003, 14:37:07 Job time: 11:9438 secs
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 20
                                                                                                                                 ORGANISM: Streptococcus suis
                                                                                                                                                                                    NAME/KEY: misc_feature;
CTHER INFORMATION: CPS2I
US-09-767-041-20
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2003, 14:21:36 ; Search time 7.33333 Seconds
 (without alignments)
 1006.744 Million cell updates/sec Run on:

US-09-508-487-21 904 1 MNKFLIVVLLAFCVFSSFAQ......DINMGQASALGFELSFKKSY 178 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

inimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

		Description	P48918 albinaria c	P39886 streptomyce	Q986r8 rhizoblum 1		O66932 aquifex aeo		P54493 bacillus su			P32482 pseudomonas	Q9i4f5 pseudomonas			Q01857 rhizobium l		o		P46105 streptomyce		P18780 alcaligenes	0			Q9piml campylobact							σn	17	P37979 synechocyst
SUMMARIES		ΠD	NU5M_ALBCO	TCMA_STRGA	DTA2_RHILO	YKE6_YEAST	PHSG_AQUAE	BXB_CLOBO	YQGP_BACSU	OOXB_AGRT4	CBBB_BACTV	CMLA_PSEAE	DCTA_PSEAE	CYOB_ECOLI	CCDA_BACSU	DCTA_RHILE	SLAP_CAMFE	YA96_MYCPN	DCTA_YERPE	AC22_STRCO	IMB4_YEAST	TERC_ALCSP	MODF_ECOLI	A1A4_HUMAN	A1A4_MOUSE	LPXA_CAMJE	MOT4_CHICK	CRP_RAT	PTKC_ECOLI	PTTB_BACSU	YWCA_BACSU	PTBA_ERWCH	NCAP_PVM	Y PUM_RHOCA	ICFG_SYNY3
		80	1	Н	П	-	Н	-	П	Н	-	Н	-	Н	Н	Н	Н	-	-	~	-	-	Η	1		-	-	Η	Н	П	7		-	-	П
		Match Length	545	538	442	449	692	1290	507	371	750	419	436	663	235	444	933	264	429	578	1113	346	490	992	1032	263	473	230	451	470	516	631	393	477	634
d	Query	Match	9.6	9.4	9.5		0.6	9.0	-	8.0	•	æ	8.7	٠.	•	8.6		8.5	8.5	8.5	8.2	8.1	8.1	8.1	8.1	8.1	•	٠	٠					8.0	8.0
		Score	86.5	82	ന	83.5	81.5	81.5	81	80.5	80	79.5	78.5	78.5	78	^	o	4.	74.5	74	74	73.5	73.5	73.5	73.5	73	73	72.5	72.5	72.5	'n	72.5	72	72	72
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Q9k537 mycobacter1 P47467 mycoplasma	P03819 escherichia P50482 orvetolagus							
YQ00_MYCPA Y225_MYCGE	KEFC_ECOLI	NAH2_HUMAN	CC47_YEAST PMP1_CHLPN	HGPA_HAEIN	RL10_RHILO	RENI_HUMAN	QOX1_BACSU	CCMF_BRAJA
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G Q	
Qy Db	123 UTRITEIIIPFTFA 136    :::    : 135 TNRLGDVLIIATFS 148

---AFKWTWGK----GMMLAGAV----TMAVT 124

96 LDKNAPKA--

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205 RAERAPKSFDVSGIVLLSGAMFCLVWGLIKAPAWGWGDLRTLGFLAAAVLAFAGFTLRES 264
                                 125 RLTEIIIPFTFANS 138
                                                               265 RATEPLMPLAMFRS 278
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                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEMBRANE ELECTROCHEMICAL GRADIENTS.
--- PATHARY: POLYKetide antibiotic tetracenomycin C biosynthesis.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: BELONGS TO THE MAJOR REALLITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                     Bacteriol. 174:3651-3658(1992).
- FUNCTION: RESISTANCE TO TETRACENOMYCIN C BY AN ACTIVE TETRACENOMYCIN C EFFLUX SYSTEM WHICH IS PROBABLY ENERGIZED BY
                                                                                                                                                                                                                                                                        Guilfoile P.G., Hutchinson C.R.;
"Sequence and transcriptional analysis of the Streptomyces glaucescens tcmAR tetracenomycin C resistance and repressor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004638; Efflux_EmrB.
InterPro; IPR003662; sub_transporter.
Pfam; PP00083; sugar_tr; 1.
IGRRAMS; TIGR00711; efflux_EmrB; 1.
Antibiotic resistance; Antibiotic biosynthesis; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.4%; Score 85; DB 1; Length 538; 4.6%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DED3F28C1F22AA56 CRC64;
                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-VIN-2002 (Rel. 41, Last annotation update)
Tetracenomycin C resistance and export protein.
                               538 AA.
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                                 PRT;
                                                                                                                                                                                                                                           STRAIN=ATCC 13032 / ETH 22794 / GI
MEDLINE-92276347; Pubmed=1592819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54846 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.68;
                                                                                                                                               Streptomyces glaucescens.
                               STANDARD;
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A41901; A41901
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538 AA;
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Matches 33; Conserv
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                                                             01-FEB-1995 (Rel.
01-FEB-1995 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                              NCBI_TaxID=1907
                               TCMA STRGA
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SEQUENCE
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                                                P39886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                    Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Isbakawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuoli C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By similarity).
SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 7:331-338(2000).

-!- FUNCTION: Responsible for the transport of dicarboxylates such a sucinate, fumarate, and malate from the periplasm across the membrane. This transport system plays an important role in the energy supply of rhizobium-legume symbionts (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inner membrane; Symport;
                                                                                                                                                   Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                 41, Last sequence update)
41, Last annotation update)
                                 442 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0173; EDTRNSPORT.
PROSITE; PS00713; NA_DICARBOXXL_SYMP_1; 1.
PROSITE; PS00714; NA_DICARBOXXL_SYMP_2; 1.
Transport; Sugar transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Mismatches
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                                                                               15-JUN-2002 (Rel. 41, Last sequence u
15-JUN-2002 (Rel. 41, Last annotation
C4-dicarboxylate transport protein 2
DCTA2 OR MLL7237.
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP003011; BAB53385.1; -.
InterPro; IPR001991; Na/diCO_symp.
Pfam; PF00375; SDF; 1.
                                                              15-JUN-2002 (Rel. 41, Created)
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                                 STANDARD:
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                                                                                                                                                                                                      NCBI_TaxID=381;
                                 DTA2_RHILO
Q986R8;
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               DTA2_RHILO
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RESULT
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Gaps

38; Indels

19; Mismatches

Conservative

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49 PFLLNLFLGFGIG----SFAQGDILGGFLI--LGFDA-----VGIGLILTGAYLDIKA 95

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PHSG_AQUAE
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Matches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
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                                                                                                                                                                                               GLGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                 80 VGIGLILTGAY---LDIKALDKNAPK-AAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 FLTFSTLALIIGLVVANVVQPGAGFNIDPATLDASTVNTYAAKAHDQSVTGFLMNIIPGT 152
                                                                                                                                                                      102 KAAF---KWTWGK---GMMLAGAVTMAVTRLTEIIIPFTFANS---YN------RKLK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purnelle B., Tettelin H., van Dyck L., Skala J., Goffeau A.; "The sequence of a 17.5 kb DNA fragment on the left arm of yeast chromosome XI identifies the protein Kinase gene ELMI, the DNA primase gene PRI2, a new gene encoding a putative histone and seven new open reading frames."
FLIVVLLAFCVFSSFAQADDSKSAFNLGA----GEKLLAYETSKKD-PIVPFLLNLFLGF
                                                                                   GIGSFAQGDILGGFLILGFDAV-GIGLILTG-------AYLDIKALDKNAP
                                                                                                                          153 IVGAFADGDIL---QVLFFSVLFGIALALVGDKGAPVLNFLQALMAPMFKLVSVLMKAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 49.6 kDa protein in ELMI-PRI2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 449;
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                                                                                                                                                                                                                                                                                                                                                                                                                        449 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 3.1;
17; Mismatches
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                                                                                                                                                                                                                                                             145 NSLNIAFGGFE----PSFDINMGQASA 167
                                                                                                                                                                                                                                                                                                       270 EELLLVLGTSSSEAALPSLMEKMEKAGA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; S0001529; YKL046C.
InterPro; IPR005198; Glyco_hydro_76.
Pfam; PF03663; Glyco_hydro_76; 1.
Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X71621; -; NOT_ANNOTATED_CDS.
EMBL; Z28046; CAA81881.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: TO YEAST YMR238W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94205268; PubMed-8154189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49565 MW;
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447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 ANSYNRKLKNSLN 148
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269 SDLWHTRTKEFLN 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S37867; S37867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                     YKE6_YEAST
P36091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYDRATE METABOLISM. ENZYMES FROM DIFFERENT SOURCES DIFFER IN THEIR REGULATORY MECHANISMS AND IN THEIR NATURAL SUBSTRATES. HOWEVER, ALL KNOWN PHOSPHORYLASES SHARE CATALYTIC AND STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 YVKQRIRVDGWQEDLDAQNQKELMPVKKVLDKEG-----KWLKCYVYVRDEKVYFGVW-- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 YETSKKDPIVPFL-----LNLFLGFGIGSFAQGDILGGFLILGFDAVGIGLILTGA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASALGF 170
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                                                                                                                                                                                                                                                                                                      Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Glycosyltransferase; Carbohydrate metabolism;
Glycogen metabolism; Pyridoxal phosphate; Complete proteome.
BINDING 586 586 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 692 AA, BILSB MW; 4DCOEA2B2ESBBEA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROPERTIES (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: {(1,4)-alpha-D-glucosyl}(N) + phosphate = {(1,4)-alpha-D-glucose 1-phosphate.}

-!- COFACTOR: PYRIDOANAL PHOSPHATE (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE GLYCOGEN PHOSPHORYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 392:353-358(1998).
-!- FUNCTION: PHOSPHORYLASE IS AN IMPORTANT ALLOSTERIC ENZYME IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycogen phosphorylase (EC 2.4.1.1).
692 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1290 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00343; phosphorylase; 1. PROSITE; PS00102; PHOSPHORYLASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000704; AAC06896.1; -.
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STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                      Aquifex aeolicus
                                                                                                                                                                                                                              OR AQ_717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P00489;
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-!- FUNCTION: BOTULING' TOXIN ACTS BY INHIBITING NEUROTRANSMITTER RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPERILDASE THAT CLEAVES THE 76-GLN-|-PHE-77 BOND OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNAPTOBREVIN-2. CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurotoxin gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION OF SUBSTRATE.
MEDLINE-93063293; PubMed=1331807;
Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,
Dasgupta B.R., Montecucco C.;
"Tetanus and botulinum-B neurotoxins block neurotransmitter release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schiavo G., Rossetto O., Santucci A., Dasgupta B.R., Montecucco C.; "Botulinum neurotoxins are zinc proteins."; J. Biol. Chem. 267:23479-23483(1992).
                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-92384550; PubMed-1514783;
Whelan S.M., Elmore M.J., Bodsworth N.J., Brehm J.K., Atkinson T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                           Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIATE = 99000987; PubMed=3139097; Dasgupta B.R., Datta A.; Botulinum neurotoxin type B (strain 657): partial sequence and similarity with tetanus toxin."; Biochimie 70:811-817(1988).
                                                                                                                                                                                                                                                                                         encoding the type B neurotoxin and determination of its entire nucleotide seminary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.;
"Partial amino acid sequences of botulinum neurotoxins types B
               01-JUL-1989 (Rel. 11, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Botulinum neurotoxin type B precursor (EC 3.4.24.69) (BONT/B)
                                                                                                                                                                                                                                                                                     'Molecular cloning of the Clostridium botulinum structural
                                                                                                                                                                                                                                                                                                                                                                                                                Szabo E.A., Pemberton J.M., Desmarchelier P.M.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campbell K., East A.K., Collins M.D.;
"Gene probes for identification of the botulinal neuroto
specific identification of neurotoxin types B, E, and F.
J. Clin. Microbiol. 31:2255-2262(1993).
                                                                                                                                                                                                                                                                                                                                      Appl. Environ. Microbiol. 58:2345-2354(1992).
[2] SEQUENCE OF 35-245 FROM N.A.
STRAIN-NCTC 7273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by proteolytic cleavage of synaptobrevin.";
Nature 359:832-835(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arch. Biochem. Biophys. 238:544-548(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=NCTC 7273;
MEDLINE=94013372; PubMed=8408542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-85197963; PubMed-3888113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93054694; PubMed-1429690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION AS ZINC-PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 633-993 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-44 AND 441-466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-16 AND 441-458.
                                                                                                                          Clostridium botulinum,
                                                                                                                                                                                                                                                                                                                         nucleotíde sequence.
                                                                                                                                                                             NCBI_TaxID=1491;
                                                                                          (Bontoxilysin B)
 P10844; P10843;
                                                                                                                                                                                                                                                                    N.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-OKRA;
                                                                                                                                                                                                                                                                                                                                                                                                              Szabo E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-657
                                                                                                                                                                                                                                                                      Minton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  619 IVPY-IGLALNVG-NETAKGNFENAFEIAGASILLEFIPELLIPVVGAFLLESYIDNKNK 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 -IKALDKNAPKAAFKWTWGKGMMLAGAVTMAVTRL-------TEIIIPFT 134
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                                                                              DISTINCT FORMS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 IVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAV------GIGLILTGAYLD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOTULINUM NEUROTOXIN B, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN B, HEAVY-CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC (CATALYTIC) (BY SIMILARITY).
INTERCHAIN (PROBABLE).
T -> M (IN REF. 4).
R -> G (IN REF. 2).
A -> S (IN REF. 2).
S -> R (IN REF. 4).
S -> R (IN REF. 4).
NW; D21746E2C024DF43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probom; P0001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56; Indels
                                                                                          BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                         SUBCELLULAR LOCATION: Secreted.
MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY
                                               FORMATION AND TOXIN BINDING, RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.0%; Score 81.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 FANSYNRKLKNSLNIAFGGFEPSFDINMGQA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 Y-NIYSEKEKSNINIDFNDINSKLNEGINQA 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000395; Bontoxilysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01742; Peptidase_M27; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150670 MW;
                                                                                                                                                                                                                                                                        EMBL, 211934; CAA77991.1; --
PMBL, X770817, CAA50148.1; --
PTR, S07128. S07128.
PTR, S07155; S07155.
PTR, S08652, S08652.
PTR, S08573; S08574.
PTR, S08574; S08574.
PTR, A48940, A48940.
HSSP, P10845; 3BTA.
MEROPS; M27.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00760; BONTOXILYSIN.
                                                                                                                                                                                                                                                             EMBL; M81186; AAA23211.1; -.
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436
29
217
224
224
263
1290 AA;
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P54493;
01-OCT-1996 (
01-OCT-1996 (
15-JUN-2002 (
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METAL
DISULFID
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YQGP_BACSU
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A Kunst F., Ogasavara N., Bessieres P., Bolotin A., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Barsiere L., Brans A., Braun M., Brignell S.C., Bron S., Brourier L., Brans A., Braun M., Brignell S.C., Bron S., Broullet S., Buschic L., Frans A., Braun M., Brignell S.C., Bron S., Broullet S., Buschic L., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entiz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Brigeppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Anderia B., Karamate D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobyashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Mone D., O'Reilly M., Portetelle D., Porwollik S., Prescott A.M., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Racer M., Rivolta C., Schleich S., Schroeter R., Scoffone F., Scholeth M., Tanakoshi H., Takamaru K., Takaul H., Wandler E., Wedler E., Weller S., Winters P., Wasaancto M. K., Yoshikawa H.F., Zamstein B., Yoshikawa H., Danchin A., Serron P., San Sondon S., Wasaancto M., Wasaancto W., Winters P., Winters P., Winters P., Winters P., Wasaancto M., Wasaancto W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W., Wasaanch W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: SOME, TO E.COLI AND H.INFLUENZAE GLPG, P.STUARTII AARA
AND YEAST YGRIOHW.
                                                                                                                                                           MEDLINE-97124195; PubMed-8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                   "systematic sequencing of the 283 kb 210 degrees-232 degrees region of
the Bacillus subtilis genome containing the skin element and many
                                              Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; Transmembrane; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98044033; PubMed-9384377;
                                                                                                                                                                                                                                                                                                        Microbiology 142:3103-3111(1996)
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Pfam; PF01694; Rhomboid; 1.
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281
303
                                                                                                                                                                                                                                                                                       sporulation genes."
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                   Bacillus subtilis
                                                                                                                 SEQUENCE FROM N.A
                                                                  NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 SDASARRWPTMANTLLDDSGIDVGLQQDGAFTFALSEEELEANRQDMESIELETNGRAPQ 124
                                                                                                                                                                                              260 RFLLIYLAAGITGSIASFVFSPYPSAGASGAIFGCLGALLYVALSNRKMFLRTIGTNIIV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 -- AGA---VIMAVIRLTEIII-----PFTFANS----YNRKLKNSLNIAFGGFEPS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                         3 KFLIVVL-----LAFCVFSSFAQADDSKSAFN-LGA-----GEKLLAYETSKKDPIV 48
                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Opine oxidase subunit B (EC 1.-.-.) (Octopine oxidase subunit B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 IIGGGLVGASIAWGLARSGTKPLVLDGADLDLRASRAN---FALVWVQGKGLHAPHYALW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schroeder J.;
"Octopine and nopaline oxidases from Ti plasmids of Agrobacterium "Octopine and nopaline oxidases from Ti plasmids of Agrobacterium tumefaciens: molecular analysis, relationship, and functional characterization.";
J. Bacteriol. 176:4511-4517(1994).
-i- FUNCTION: OXIDATIVE CLEAVAGE OF OCTOPINE INTO L-ARGININE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens (strain Ach5).
Plasmid pTiAch5.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-94321320; Pubmed-8045881;
Zanker H., Lurz G., Langridge U., Langridge P., Kreusch D.,
                                                                         Similarity 28.3%; Pred. No. 5.8; Schmilarity 28.3%; Pred. No. 5.8; Onservative 17; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                ::|| || :: || || || || || || || || || 320 IIIINLGFGFAVSNIDNSGHIGGLIGGF----FAAAALGLPKAGAF 361
POTENTIAL.
POTENTIAL.
7FDF65D4EB2C81E5 CRC64;
                                                                                                                                                                                                                                       49 PFLLNLFLGFGIGSFAQ----GDILGGFLILGFDAVGIGLILTGAY 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 AA; 39939 MW; 948705136822AC52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRUVATE (BY SIMILARITY).
-!- PATHWAY: CATABOLIC UTILIZATION OF OCTOPINE.
-!- SUBUNIT: HETERODIMER OF A SUBUNIT AND A B SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
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30.9%; Pred. No. 4.7;
tive 13; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                             371 AA
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InterPro; IPR000205; NAD_binding.
Pfam; PF01266; DAO; I.
Oxidoreductase; Plasmid.
                                    56439 MW;
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Best Local Similarity
Matches 38; Conserva
312
365
307 AA;
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Q59159;
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Best Local
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REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                              P SEQUENCE FROM N.A.

P STRAIN-CIB 163-131;

E STRAIN-CIB 163-131;

MEDLINE-98449784; PubMed-9774743;

MEDLINE-98449784; PROMOGES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT SETHELLAL CELLS OF MOSQUITOS SUCH AS. AEDES AEGYPII, ANOPHELES ALBIMANUS AND:CULEX QUINQUEFASCIATUS LARVAE.

MEDLIAMANUS AND:CULEX QUINQUEFASCIATUS LARVAE.
                                                                                                             16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cryllBb (Insecticidal delta-endotoxin CryXIB(b)) (Crystaline entomocidal protoxin) (84 kDa crystal protein).
CRYLIBB OR CRYXIB(B)
Bacillus thuringiensis (subsp. medellin).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 GAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASALGFELSFKK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----FDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578 GGIPVEGNSGWVDYITDSFTFNDLGITTASTNAFFSI----DSDGVNASQQWYLSKLILVK 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 FSSFAQADDSKSAFNLGAGEKLLAYETSKK-DPIVPFLLNLFLGFGIGSFAQGD----IL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523 FTETVLGNEAKYSIRLNTG----FNTATRYRLVIRFKATARLAAGIRVRSQNSGNNRLL
                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%; Score 80; DB 1; Length 750; 0.3%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     750 AA; 84407 MW; 293C383018B33D46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY
                                                                          750 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001178; Endotoxin.
                                                                                                   (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF017416; AAC97162.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00555; endotoxin; 1. Toxin; Sporulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                     NCBI_TaxID=79672;
                                                                                                                                                                                                                                                                                                                                                                                                             N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGFLILG--
|::
125 FEV 127
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Local Sim.
37;
                                                                                                   16-0CT-2001
                                                                        CBBB_BACTV
09ZIU5;
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CMLA_PSEAE
ID CMLA_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                              CBBB_BACTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             693
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                                                 RESULT 9
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TRANSPOSON-TIL696,
MEDLINE-91294195; Pubmed-1648560;
MEDLINE-91294195; Pubmed-1648560;
MEDLINE-1294195; Pubmed-1648560;
MEDLINE-91294195; Pubmed-1648560;
Characterization of the nonenzymatic chloramphenical resistance
(cmlA) gene of the In4 integron of Tn1696; similarity of the product
(cmlA) gene of the proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Partridge S., Hall R.M.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: IT APPEARS TO PROVOKE A REDUCTION OF THE CONTENT OF

-!- SUBCELLIDIAR LOCATION: Integral membrane protein. Inner membrane.

-!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY). BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pir; A7033; A4703.
InterPro; IPR004734; Drug_resist.
InterPro; IPR004012; Efflux_Bcr_CflA.
InterPro; IPR003662; Bub_transporter.
Pfam; PF00083; sugar_tr; 1.
TIGRFMAS; TIGR00710; efflux_Bcr_CflA; 1.
TIGRRAMS; TIGR00880; 2_A_01_02; 1.
Antibiotic resistance; Transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of the inducible chloramphenicol resistance determinant in the Th1696 integron suggests regulation by translational attenuation."; Plasmid 26:10-19(1991).
                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
P32482; Q56411; Q56412;
01-007-1993 (Rel. 27, Created)
10-007-1993 (Rel. 27, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                     Chloramphenicol resistance protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TARANSPOSON—TIL696,
MEDLINE=9205679; PubMed=1658833;
Stokes H.W., Hall R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid; Transposable element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U12338; AAB60004.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M64556; AAA26057.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCR/CMLA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
30
46
67
80
1101
1127
1141
1162
214
                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSPOSON-Tn1696;
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=287;
                                                                                                                                                                                                                 Plasmid R1033.
                                                                                                                                                                                                                                                                           Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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-I- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 WLYTLCYAAGMGSFFVFFSIAPGLMMGRQGVSQLGFSLL-FATVAIAMVFTARFMG---- 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 DKNAPKAAFKW-----TWGKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ALQSV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 FLLNLFLGFGGGSF-----AQGDILG-----GFLILGFDAVGIGLILTGAYLDIKAL 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity).
SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X. O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Couller S.N., Polger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 419;
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
8 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
9 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
10 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38; Indels
                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
12 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                       B5BF1D97DD7B9798 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C4-dicarboxylate transport protein.
                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                         8.8%; Score 79.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                       44243 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       23.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 FGGFEPSFDINMGQASAL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | : : : | |:|
308 LGFIAPMWLVGIGVATAV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa.
                                                              (SDF, TC 2.A.23).
                                                                                                                                                                                                                                                                                                                                                 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                   280
300
307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCTA_PSEAE
Q914F5;
                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                                    TRANSMEM
                                                              PRANSMEM
                                                                                                                      FRANSMEM
                                                                                                                                                                                                                                                                                            FRANSMEM
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        TRANSMEM
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                                                                                           DOMAIN
                                                                                                                                                                                                      DOMAIN
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1D DCTA_PSEAB

1D DCTA_PSEAB

DD DCTA_PSEAB

DT 15-JUN.

DT 15-JUN.

DT 15-JUN.

DT 15-JUN.

DE C4-dice

GN DCTA OF CO.

DSEUGON

CO PSEUGON

CO C -1-FUN

                                                                                                                                                                                                                                                                                                                        OMAIN
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-3002 (Rel. 41, Last annotation update)
Ubiquinol oxidase polypeptide I (EC 1.10.3.) (Cytochrome O subunit 1)
(Oxidase BO(3) subunit 1) (Cytochrome O ubiquinol oxidase subunit 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chepuri V., Lemieux L., Au D.C.T., Gennis R.B.;
"The sequence of the cyo operon indicates substantial structural
similarities between the cytochrome o ubiquinol oxidase of
Escherichia coli and the aa3-type family of cytochrome c oxidases.";
J. Biol. Chem. 265:11185-11192(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 DDSKSAFNLGAGEKLLAYETSKKDPIVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAV- 80
EMBL, AE004548; AAG04572.1; -.
InterPro: IPR001919; Na/dico_symp.
Prfam; PF00375; SDF; 1.
PRINTS; PR00173; EDTRNSPORT.
PROSTITE; PS00713; Na_DICARBOXXL_SYMP_1; FALSE_NEG.
PROSTITE; PS00713; Na_DICARBOXXL_SYMP_2; 1.
Transport; Sugar transport; Transmembrane; Symport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-KIZ. / MG165;
STRAIN-KIZ. / MG165;
BEDALINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
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Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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Escherichia.
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MEDLINE-90293062; PubMed-2162835;
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TRANSMEM 9
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                           ASP-75; HIS-98 AND GLN-101.

ASP-75; HIS-98 AND GLN-101.

ASP-75; HIS-98 AND GLN-101.

AND MEDLINE-2047333; PubMed-11017202;

Abramson J., Riistama S., Mikstrom M.;

Puustinen A., Iwata S., Wikstrom M.;

"The structure of the ubiquinol oxidase from Escherichia coli and its ubiquinone binding site.";

"The Struct. Biol. 7:910-917(2000).

-I FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT OF THE ARROGHED THE ARRATORY CHAIN OF E.COLI THAT PREDOMINATES WHEN CELLS ARE GROWN AT HIGH ARRATORY THIS UBIQUINOL OXIDASE SHOWS PROTON PUMP ACTIVITY ACROSS THE MEMBRANE IN ADDITION TO THE
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-!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chepuri V., Gennis R.B.; "The use of gene fusions to determine the topology of all of the subunits of the cytochrome o terminal oxidase complex of Escherichia
       STRAIN-0157:H7, EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
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MEDLINE-90330636; PubMed-2165491;
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EMBL; AE000149; AAC73534.1; -.
EMBL; U82664; AAB40187.1; -.
EMBL; AE005222; AAG54781.1; -.
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3D-structure; Complete proteome.
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R->Q: ABOLISHES ENZYME ACTIVITY.
D->N: ABOLISHES ENZYME ACTIVITY.
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Q->N: REDUCES ENZYME ACTIVITY BY
17357BBD44C7CF84 CRC64;
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ECGGENE; EG10179; CyOB.
InterPro; IPR000883; COXI.
Pfam; PF00115; COXI; 1.
PROSITE; PR01165; CYCOXIDASEI.
PROSITE; PR01077; COXI; 1.
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EMBL; AP002551; BAB33908.1;
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RESULT 13

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                                                                                                                                                                                                                                    "New genes in the 170 degrees region of the Bacillus subtilis genome encode DNA gyrase subunits, a thioredoxin, a xylanase and an amino
                                                                                                                                                                                                                                                                                                                                            MEDLINE-97221596; PubMed-9068642; Schloett T., von Wachenfeldt C., Hederstedt L.; "Identification and characterization of the ccdA gene, required for cytochrome c synthesis in Bacillus subtilis."; J. Bacteriol. 179:1962-1973(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schloett T., Hederstedt L.; "Efficient spore synthesis in Bacillus subtilis depends on the CcdA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.";
J. Bacteriol. 182:2845-2854(2000).
-I- FUNCTION: REQUIRED FOR CYTOCHROME C SYNTHESIS AND STAGE V OF SPORULATION. MIGHT TRANSFER REDUCING EQUIVALENTS ACROSS THE
                                                                                                                                   Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                     01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome c-type biogenesis protein ccdA.
            235 AA.
              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION, AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20245543; PubMed-10781554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
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                                          Created)
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            STANDARD;
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                                                                                                                   Bacillus subtilis.
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                                                                                                                                                                                                                                                                        transporter.
                                                                                                                                              NCBI_TaxID-1423;
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Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1991) to the transport of dicarboxylates such as election to the transport of dicarboxylates such as succinate, fumarate, and malate from the periplasm across the inner membrane. This transport system plays an important role in the energy supply of rhizobium-legume symbionts (By similarity). 68 I------LGGFLILGFDAVGIGLILTGAYLDIKALD-KNAPKA------AF 105 80 LFRDYHDAIRQIGALLIILFGFITLGVFRPEAMMKERRIHFKHKPSGFLGSVLIGMAFAA 139 106 KWTWGKGMMLAGAVTMAVTR------LTEIIIPFTFANSYNRKL----KNSLNIA 150 48; Gaps 28 AFLSYITGVSMDDVKT-----EKLLLQKRSLFHTLC-FLLGFSVIFIALGYGTSFIGS 79 CYTOPLASMIC MEMBRANE, PROMOTING EFFICIENT DISULFIDE BOND ISOMERIZATION OF PROTEINS LOCALIZED ON THE OUTER SURFACE OF THE MEMBRANE OR IN THE SPORE COAT. 11 AFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKKDPIVPFLLN---LFLGFGIGSFAQGD Bacteria; Proteobacteria; aĺpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium. Length 235; Cytochrome c-type biogenesis; Sporulation; Transmembrane; Indels D94F3E62EDD2AC29 CRC64; PATHWAY: CYTOCHROME C SYNTHESIS SYSTEM II. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE DSBD SUBFAMILY. 25; Mismatches 67; DB 1; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 444 AA. POTENTIAL. POTENTIAL. Score 78; Pred. No. POTENTIAL POTENTIAL POTENTIAL C4-dicarboxylate transport protein. Ctytoch_TM. EMBL; 273234; CAA97594.1; -.
EMBL; X87845; CAA61116.1; -.
EMBL; 299113; CAB13677.1; -.
Subtilist; BG11240; ccda.
InterPro: IPR003834; Ctytoch_TP Pfam; PF02683; Dsbb; 1. 26007 MW;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 FLNSLTAPVFKLVAILMKAAPIGAFGAMAFTIGKYGVGSIANLAMLIG--TFYITSLLFV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 AHEQS----IVGFLTNIIPTTIVGAFADGDIL---QVLFFSVLFGIALAMVGEKGEQVVN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 AYETSKKDPIVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAV-GIGLILTG------ 88
                       -1 - SIMILATITY: BELONGS TO THE SODIUM: DICARBOXYLATE SYMPORTER FAMILY (SDF, TC 2.A.23).
                                                                                                                                                                        EMBL; 211529; CAA77618.1; -
PIR; S25701; S25701.
PIR; S27801; S2701.
PIR; S27804; S27801.
PIN S27801.
PRO0191; Na/dicO_symp.
PROSITE; PS00713; Na_DICARBOXYL_SYMP_1; 1.
PROSITE; PS00714; Na_DICARBOXYL_SYMP_2; 1.
Transport; Sugar transport; Transmembrane; Inner membrane; Symport.
TRANSMEM 18 40
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campylobacter fetus.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
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MEDLINE-90354448; PubMed-2387868;
Blaser M.J., Gotschlich E.C.;
"Surface array protein of Campylobacter fetus. Cloning and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     AA2A5EA9E6780653 CRC64;
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01-OCT-1994 (Rel. 30, Last annotation update)
S-layer protein (Surface array protein) (SAP)
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29.1%; Pred. No. 10;
tive 15; Mismatches
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J. Biol. Chem. 265:14529-14535(1990)
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J. Biol. Chem. 265:19372-19372(1990).
-!- FUNCTION: THE S-LAXER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
CRITICAL FOR VIRULENCE.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH HEXAGONAL SYMMETRY.
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24.6%; Pred. No. 26;
iive 21; Mismatches
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nes 42; Conservative
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March 14, 2003, 14:22:51 ; Search time 24.3333 Seconds
   (without alignments)
1507.249 Million cell updates/sec
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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904
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inimum DB seq length: 0 aximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:* Database :

sp_archea:*
sp_bacteria:*
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sp_human:*
sp_lnvertebrate:*
sp_mammal:* sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_rvirus:* sp_bacteriap:* sp_organelle:* sp_phage:* sp_rodent:* sp_plant: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:

Q9x3u9 borrella af Q9x3v0 borrella ga O51065 borrella bu O50896 borrella bu O50896 borrella bu O5019 borrella bu O51143 borrella bu Q93125 borrella bu Q93166 vibrio para Q971ev Zebbocteri Q971ev Clostridium Q971ev Clostridium Q971ev Glostridium Q971ev Glostridium Q971ev Glostridium Q971ev Glostridium Q971ev Glostridium Q971ev Allocobacteri Q92mt7 helicobacteri Description SUMMARIES Q9X3V9 Q9X3V0 O51065 O50896 O50696 O50696 Q9S011 O31325 Q31325 Q3166Q Q9FDM0 Q97JE7 Q9RTD0 Q8UAV6 Q9ZMT7 DB Length Query Match Score 904 786.5 769.5 293.5 240 240 237 160 95.5 90 90 89.5 88 87.5 Result Š

09hhi2 halobacteri 0929n4 listeria in 089260 listeria mo 090w87 candida alb 097re5 streptococc p73100 synechocyst 09kpp3 bacillus ha 024796 echinococcu 005768 echinococcu 097697 sulfolobus 055742 synechocyst 07555 helicobacte 066804 aquifex aeo 058555 helicobacte 066804 aquifex aeo 058555 helicobacte 06804 aquifex aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq5 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 09xq6 oryza aeo 00xq6 oryza ae	Q9kjy5 klebsiella Q9kf96 bacillus ha Q8u2x3 pyrococcus O80918 arabidopsis
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## ALIGNMENTS

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STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
Noppa L., Ostberg Y., Bergstrom S.;
"P13, a novel integral membrane protein of Lyme disease Borrelia.";
                                                                                                                                                                                                                                                                                                                                                                                                                        121 MAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASALGFELSFKKSY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-1990;
MEDLINE-21189251; PubMed-11292755;
MEDLINE-21189251; PubMed-11292755;
MEDLINE-21189251; PubMed-11292755;
MEDLINE-21189251; PubMed-11292755;
Pl3, an integral membrane protein of Borrelia burgdorferi, is (reminally processed and contains surface-exposed domains.";
Infect. Immun. 69:3323-3334 (2001).
EMBL; AF085741, AAD28362.1;
SEOUENCE 177 AA; 19308 MW; 429928CC426E1111 CRC64;
                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                Length 177;
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                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                      Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID-29519;
                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi (Lyme disease spirochete).
Bacteria, Spirochaetales, Spirochaetaceae, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                               87.0%; Score 786.5; DB 2;
86.5%; Pred. No. 2.1e-63;
tive 7; Mismatches 16;
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                                 177 AA
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                                                      12,
12,
19,
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Matches 154; Conservative
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                                PRELIMINARY;
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                                                   01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                             01-DEC-2001 (TrEMBLrel.
                                                                                          Membrane protein P13
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                                                                                                                Borrelia garinii
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SEQUENCE FROM N.A.

STRAIN-ATCC 35210 / B31;

MEDLINE-98065943; PubMed-9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,

Lathjgra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,

Van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

Utterback T., Watthey L., McDonald L., Artlach P., Bowman C.,

Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,

Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITKRAAFQWTWGKGVMLAGVV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                     60 IGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAV 119
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                                                                                                                                                                                                  85.1%; Score 769.5; DB 16; Length
84.9%; Pred. No. 7.3e-62;
.ive 10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic sequence of a Lyme disease spirochaete, Borrelia
(AUG-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                           Hypothetical protein; Complete proteome.
SEQUENCE 179 AA; 19104 MW; FD6056E8E24E5D5D CRC64;
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SEQUENCE 161 AA; 17887 MW; D93BDB326FE2DA30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Spirochaetales; Spirochaetaceae; Borrella.
NCBL_TaxID-139;
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20, Last annotation update)
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ilarity 41.1%; Pred. No. 6.1e-19;
Conservative 24; Mismatches 61
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Nature 390:580-586(1997).
EMBL; AE000790; AAC66226.1;
                       EMBL; AE001117; AAC66426.1;
EMBL; AF085739; AAD28360.1;
TIGR; BB0034; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein BBA01.
                                                                                                                                                                                                                               Best_Local Similarity 84.99
Matches 152; Conservative
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Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
                                                                                                "Genomic sequence of a Lyme disease spirochaete, Borrella burgdorferi.";
burgdorferi.";
burgdorferi.";
burgdorferi.";
EMBL; ARC65989.1; -.
TIGR; BBH41; --
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Best Local Similarity
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SETAINA—ATCS 35210 / B31:
MEDLINE—98065943; PubMed—9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Ulterback T., Watthey L., McDonald L., Artlach P., Bowman C.,
Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B.,
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STRAIR-ATCC 35210 / B31;
MEDLINE-B065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathjgra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlawage A.N., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
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38.8%; Pred. No. 3.8e-18;
iive 25; Mismatches 70; Indels 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 170 AA; 18227 MW; 0E71B633EA80FB22 CRC64;
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Bacteria: Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBL_TaxID=139;
                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein BBH41.
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                                                                                                          170 AA
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EMBL; AE000789; AAC66194.1; -.
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Best Local Similarity 38.8%
Matches 69; Conservative
                                                                                                          PRELIMINARY;
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Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Lathigra R., Fraser C.M., Casjens S., Hickey E.K., Gwinn M., Peterson J., van-Vugt R., White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-Vugt R., Balmer N., Haft D., Rosa P., Stevenson B.; "A bacterial genome in flux: The twelve linear and nine circular extractromosomal DNAs in an infectious isolate of the Lyme disease spirochete Borrella burgdorferi."; Morrobote Borrella burgdorferi."; EMBL; AE001584: AAF0770:1; -. 95 ALDKNAPKAAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGF 154 76 GFDAVGIGLILTGAYL--DIKALDKNAPKAAFKWTWGKGMMLA--GAVTMAVTRLTEIII 131 Gaps 18; Gaps 18 FAQADDSKSAFNLGAGE--KLLAYETSKKDPIVPFLLNLFLGFGIGSFAQGDILGGFLIL 75 36 LLAYETSKK-DPIVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAVGIGLLLTGAYLDIK 94 4 FAQEKLEK-----GVGDIATVMKYESKKATILAPLLLNIFLSLGIGSFVQGDYIGGGALL 12; tch 26.5%; Score 240; DB 16; Length 190; al Similarity 39.6%; Pred. No. 5e-14; 57; Conservative 23; Mismatches 52; Indels 1 Length 161; 49; Indels Plasmid; Hypothetical protein; Complete proteome. SEQUENCE 190 AA; 21813 MW; A80FB8BCAD4B13EB CRC64; Hypothetical protein; Plasmid. SEQUENCE 161 AA; 17016 MW; 14D4906CC8107CD2 CRC64; Plasmid 1p56. Bacteria; Spirochaetales; Spirochaetaceae; Borrelia 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 26.2%; Score 237; DB 2; 39.7%; Pred. No. 7.7e-14; iive 24; Mismatches 49;

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25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 GFEPSFDINMGQASALG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 :: |||| ;
233 LF--AYHAIMGQAGVQG 247
  55; Conservative
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Matches 50; Conservative
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1093RE
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Q8REW2
  Matches
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SETRAIN—ATCC 35210 / B31;

MEDLINE—98065943; PubMed—9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,

Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

Dougherty B., Tomb J.F., Fleistohman R.D., Richardson D.,

Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,

van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

Utterbock T., Watthey L., McDonald L., Artiach P., Bowman C.,

Salland S., Fulil C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNKFLIVVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKKDPIVPFLLNLFLGFGI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PTS system, maltose and glucose-specific IIABC component (MALX).
BB0116.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.7%; Score 160; DB 2; Length 95;
44.4%; Pred. No. 3.8e-07;
tive 12; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5CB04166E9DA8D67 CRC64;
                                                                                                                                                                                                                                                                                                Feng S., Das S., Barthold S.W., Fikrig E.;
Feng S., Das S., Barthold S.W., Fikrig E.;
"Characterization of two genes, pll and p5, on the Bouburgdorferi 49-kilo base linear plasmid.";
Biochim. Blophys. Acta 1307:270-272(1996).
EMBL; L41151; AAB62281.1;
SEQUENCE 95 AA; 10739 WW; D12F6791F8920C3A CRC64;
                                                                                                                                                             Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spirochaetales; Spirochaetaceae; Borrelia
                                                                  Last sequence update)
Last annotation update)
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Pred. No. 1.9;
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95 AA.
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                                              Created)
  PRT;
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EMBL: AEO01124; AAC66516.1; -.
HSSP; P05053; 11BA.
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InterPro; IPR003352; PTS_EIIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSFAQGDILGGFLILGFDAVG 81
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                                         01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 44.48 tes 36; Conservative
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fam; PF02378; PTS_EIIC;
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PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                 (clone 8) s3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
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                                                                                                                                                                                                                                                                      79 AVGIGLILTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTFANS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 -PFLLNLFLGFGIGS--FAQGDILGGFLILGFDAVG----IGLILTGAYLDIKALDKNA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 PKAAFKWTW------GKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFG 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 MVFAALAVCLFVFFPQPIMGLTIDSQEVIELGSSYLVISSASMFAVACVASMAVGLRAMH 132
Gaps
                                                                                                         188 IVIILPFCVFLAIFFCLIWSSF---DDLIASLGLFVFRFEYFGSFLYGFLNRLLLPLGLH 244
                                                      6 IVVLLAFCVF-----SSFAQADDSKSAFNLGA-----GEKLLAYETSKKDPI--- 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----VPF-----DILGGF-LILGFD
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NCBI_TaxID=670;
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69
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67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Indels
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Akeda Y., Honda T.;

"Vibrio parahaemolyticus adhesin gene.";

"Ubrio parahaemolyticus adhesin gene.";

Submitted (407-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB047560; BAB59008.1; -.

InterPro; IPR002528; MatE.

Pfam; PF01554; UPF0013; 2.

TIGRRAMS; TIGRRO0797; matE; 1.

SEQUENCE 427 AA; 45909 MW; 0B608B9DC70E3C71 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   139 YNRKLKNSLNIAFGGF----EPSFDINMGQASALGF 170
                                                                                                                                                                                                                                                                                                                                                                                                                     350 FTAPLLYFVHAAYSGFALLLANFFNVTIGNSFSTGF 385
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Mismatches
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01-JUN-2002 (TrEMBLrel. 21, C;
01-JUN-2002 (TrEMBLrel. 21, Ls
01-JUN-2002 (TrEMBLrel. 21, Ls
CbiB protein.
FN0975.
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7 VVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKKDPIVPFLLNLFLGFGIGSFAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OFRIDO: 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2002 (TrEMBLrel. 21, Last annotation update) Phospho-N-acetylmuramoyl-pentapeptide-transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą.
                                                                                                                                                                    469 AA
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
SEQUENCE 469 AA; 50482 MW;
                                                                                                                                                                                                                                               Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 25.13
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                     PRELIMINARY;
                                                                                           124 TRLTEIIIP 132
                                                                                                               197 LFCSMMMLP 205
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9RTD0
                                                                                                                                                RESULT 13
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                                                                                                                                                                                                                                                                                                                                  ----KNAPKAAFKWTWGKGMMLAGAVTMAVTRLTEIIIPF-TFANSYNRKLKNSLNIAFG 152
                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                        40 -ETSKKDPIVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALD- 97
                                                                   Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasitva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.; "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586.";

EMBL; AE010604; AAL95171.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                 10.0%; Score 90; DB 16; Length 325; 23.2%; Pred. No. 3.2; ative 29; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.0%; Score 90; DB 2; Length 479; 22.5%; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Indels
                                                                                                                                                                              325 AA; 36409 MW; 9A53AE0C089DBAEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479 AA; 52095 MW; 614B052B61AD2A12 CRC64;
                                                                                                                                                                                                                                             4 FLIVVLLAFCVFSSFAQADDSKSAF-----NLGAGEKLLAY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metabolite transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            153 GFEPSFDINMGQ----ASALGFELSFKKSY 178
                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
                                                         MEDLINE-21886394; PubMed-11889109;
                                                                                                                                                                                                            Best Local Similarity 23.2%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                    FROM N.A.
FCC 25586;
                                                                                                                                                                    Complete proteome. SEQUENCE 325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=542;
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DEGLEME FROM N.A.

STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed=11466286;

MeDLINE-21359325; PubMed=11466286;

MeDLING J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin B.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing

bacterium Clostridium acetobutylicum.";

J. Bacterium 183:48234838(2001).

EMBL, AR007645; ARX79377.1;

InterPro; IPR003663; CHL-Iransport.

InterPro; IRR003663; CHL-Iransport. | | | | :|| ||| ||:| ||:| |:| |:|: :|| |:|: |:|: |:|: |:|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|:|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: 59 GIGSFAQGDILG----GFLILGFDAVGIG--LILTGAYLDIKALDKNAPKAAFKWTWGK- 111 DILGGFLILGFDAVGIGLI----LTGAYLDIKALDKNAPKAAFKWTWGKGMMLAGAVTMAV 123 Gaps 28 11 LLFIVLISCA-------AGLGGLLYGYDTAVISGAIGFLKKLYNLSPAMQGF 39; Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium. NCBL_TaxID=1488; 9.9%; Score 89.5; DB 16; Length 469; 25.1%; Pred. No. 5.3; ive 26; Mismatches 66; Indels 39. --GMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNI-AFGGFEPSFDINMG 5 LIVVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKKDPIVPFLLNLF. CDE33E2CD2A7B0DA CRC64; 01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2002 (TrEMBLrel. 21, Last annotation update)
Possible sugar-proton symporter.
CAC1339 Pfan: FF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRASPORT.
TIGRFAMS; TIGROBOT99; SF; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.

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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 FLIVVLLAF---CVFSSFAQADDSKSAFNL--------GAGEKLL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 AYETSKKDPIVPFLLNLFLGFGIGSFAQGDILGGFLILG----FDAVGIGLILTGAYLDI 93
                                                                                                                                           MEDLINE-20036896; PubMed-10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 KALDKNAPKAAFKWTWGKGMMLAG------AVTMAVTRLTEIIIPFTFANSY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales; Deinococcaceae; Deinococcus. NCBL_TaxID=1299;
                                                                                                                                                                                                                                                                                               'Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Indels
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000715; Glycos_transf_4.
InterPro; IPR003524; PNGoP_transf.
PROSITE; PS01347; MRAY_1; UNKNOWN_1.
PROSITE; PS01347; MRAY_2; UNKNOWN_1.
PROSITE; PS01348; MRAY_2; UNKNOWN_1.
Transferase; Complete proteome.
SEQUENCE 312 AA; 33450 MW; 3A284b58E9395B2F CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ABC transporter, membrane spanning protein.
ATU3261 OR AGR_L_3113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.7%; Score 88; DB 1
22.7%; Pred. No. 4.6;
ative 26; Mismatches
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TIGR; DR1835; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 22.7 les 40; Conservative
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NCBI_TaxID=176299;
                 Deinococcus radiodurans
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  radiodurans R1
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MEDLINE=21608551; PubMed=11743194;
MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 FLILATATNLSVGSL----LVGGFFAGGLMAVCLGVAI----HLSVRSVD-TLPRATGAER 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 -FLLNLFLGFGIGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPKA--AFK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 LLTSVLFSGASGSSVANAAFGASTFQPELVKHGYPPAQAGAIIAA--TSVLDNVIPPSIA 358
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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22.0%; Pred. No. 11;
iive 35; Mismatches 71; Indels 43;
                                                                                                                                                                                                                  "Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                         63402 MW; A6005D4347ABE060 CRC64;
                                                                                                                                                                                                                                                                                EMBL; AE009255; AAL44077.1; -. EMBL; AE008358; AAK90129.1; -.
                Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                        42; Conservative
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468 RQSAGEAAAIG 478
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Search completed: March 14, 2003, 14:27:04 Job time: 26.3333 secs

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Sequence 22, Appl Sequence 29, Appl Sequence 20, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 5, Appl Sequence 5, Appl Sequence 2, Appl Sequence 3, Appl Sequence 2, Appl Sequence 3, Appl Sequence 3, Appl Sequence 34, Appl Sequence 34, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 25, Appl Sequence 38, Appl Sequence 38, Appl Sequence 33, Appl Sequence 33, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence
                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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904
1 MNKFLIVVLLAFCVFSSFAQ......DINMGQASALGFELSFKKSY 178
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
version 5.1.4_p5_4578 - 2003 Compugen Ltd.
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US-09-205-987A-5
US-09-205-987A-5
US-09-205-200-25
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US-09-232-200-33
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Maximum Match 100%
Listing first 45 summaries
                                                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
  GenCore
Copyright (c) 1993
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Maximum DB seq length: 2000000000
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Sequence:
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47, Appl 59, Appl 32, Appl 32, Appl 33, Appl 43, Appl 47, Appl 559, Appl 559, Appl 66, Appl 559, Appl 66, Appl 313, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl 65, Appl		Gaps
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67.5 7.5 646 4 US-09-232-197-47 67.5 646 4 US-09-232-197-59 67.5 7.5 646 4 US-09-232-201-25 67.5 7.5 646 4 US-09-232-201-25 67.5 7.5 646 4 US-09-232-201-32 67.5 7.5 646 4 US-09-232-201-43 67.5 7.5 646 4 US-09-232-201-47 67.5 7.5 646 4 US-09-232-201-47 67.5 7.5 934 1 US-09-232-201-59 67.5 7.5 934 1 US-09-232-201-59 66.5 7.4 646 4 US-09-134-001C-5590 66.5 7.4 646 4 US-09-132-200-65 66.5 7.4 646 4 US-09-232-197-35 66.5 7.4 646 4 US-09-232-197-35 66.5 7.4 646 4 US-09-232-197-35 66.5 7.4 646 4 US-09-232-197-92 66.5 7.4 646 4 US-09-232-197-92	ALIGNMENTS  pplication US/0925829 1617 Shone, Clifford Charles Quinn, Conrad Padraig FOSTER: Keith Alan FOSTER: Keith Alan FOSTER: Keith Alan TE COMPATION: Recombinant Toxin Fragments EQUENCES: 29 NCE ADDRESS: 1100 NEW YORK AVENUE, NW, SUITE 600 SHINGTON STERNE, RESSLER, GOLDSTEIN, & FOX P. 1100 NEW YORK AVENUE, NW, SUITE 600 SHINGTON OF STERNE: POSS/MS-DOS SYSTER: PLOPPY disk IBM PC compatible SYSTER: PCOS/MS-DOS PE: Floppy disk IBM PC compatible SYSTER: PCOS/MS-DOS PATENTIN PCT/CB997/02273 TE: 23-REB-1999 CATION DATA: ON NUMBER: US 08/782,893 TE: 22-AUG-1997 CATION DATA: ON NUMBER: 132,893 TOON NUMBER: 132,893 TOON NUMBER: 132,893 TOON TOON TOON TOON TOON TOON TOON TOON	9.0%; Score 81.5; DB 4; rity 23.8%; Pred. No. 0.64; nservative 24; Mismatches 56;
2008 3008 3008 3008 3008 3008 3008 3008	RESULT 1 US-09-25-829-22 Sequence 22, A Patent No. 646 GENERAL INFOR APPLICANT: APPLICANT: APPLICANT: TITLE OF IN NUMBER OF S CORRESPONDE STATE: CORPESSEE STATE: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMPUTER: COMP	Query Match Best Local Matches

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    ---GIGLILTGAYLD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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Patent No. 6461617
GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TILLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                          -IKALDKNAPKAAFKWTWGKGMMLAGAVTMAVTRL-----
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23.8%; Pred. No. 0.64
tive 24; Mismatches
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REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0130002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
47 IVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAV-
                                                                                                                                                    135 FANSYNRKLKNSLNIAFGGFEPSFDINMGQA 165
                                                                                                                                                                              38 Y-NIYSEKEKSNINIDFNDINSKLNEGINQA 767
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FILING DATE: 23-FEB-1999
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997
APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
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Matches 36; Conservative
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MEDIUM TYPE: Floppy
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; Sequence 4175, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    678 IIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKALNYQAQALEEIIKYR 737
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                                                                                                                                                                                                                           ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                    Recombinant Toxin Fragments
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FILING DATE: 23-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997
PRIOR APPLICATION NUMBER: US/08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                Sequence 20, Application US/09255829
Patent No. 6461617
GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: ESMOND, ROBERT W. REGISTRATION NUMBER: 32,893
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
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INFORMATION FOR SEQ ID NO: 20:
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MEDIUM TYPE: Floppy
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ZIP: 20005-3934
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Matches 36; Conserv
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US-09-134-001C-4175
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                   US-09-255-829-20
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RESULT 3
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LENGTH: 451 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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: New Jersey
RY: USA
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                    131 IP-----
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                                                            ; STRAIN: F
US-08-679-635A-2
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US-09-419-163-2
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Patent No. 5985643
GENERAL INFORMATION:
APPLICANT: Tomasz, Alexander
APPLICANT: Delencastre, Herminia
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 DKLLPY----KAPFYPVGPIIVLFTLLFLLGSSFGSIASGDILG--VIRNFTPLFILAI 316
                                                                                                                                                                                                                                                                                                                                                                                                                   ::|:||: |:::| :::||1|1|209 XIIIVLV--IVYANF----NANAVFNLLNIIGSMVIVVWGSSIWSQIRLRQAIKKQGKNP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 EKLLAYETSKKDPIVPF-----LUNLFLGFGIGSFAQGDILGGFLILGFDAVGIGLI 85
EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                         8.0%; Score 72; DB 4; Length 344; 27.9%; Pred. No. 2.4; Live 16; Mismatches 27; Indels
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COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,635A
FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26.742
...DEGISTRATION NUMBER: 26.742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                         4 FLIVVLLAFCVFSSFAQADDSKSAFNL-------GAG----
               FILE REFERENCE: GTC-007
CURRENT APPLICATION WUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PALICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-114
NUMBER: OF SEQ ID NOS: 5674
LENGTH: 344
                                                                                                                                                                                                                                             ORGANISM: Staphylococcus epidermidis US-09-134-001C-4175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.yw
...hes 36; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
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STATE: New Jersey
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317 IYIAHKLIK 325
TITLE OF INVENTION:
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GENERAL INFORMATION:
APPLICANT: Tomasz, Alexander
APPLICANT: Tomasz, Alexander
APPLICANT: Delencastre, Herminia
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                           77 GIISTPGVAYLIRDMGAELGVMISASHNPVADNGIKFFGSDGFKLSDEQENEIEALLDQE 136
                                                                                                                                                                                                                                                                                     23 AFKLGRYGGYVLAHNKGEKHP-----RVLVGRDTRVSGEMLESALIAGLISIGAEVMRL 76
                                                                                                                                                                                            38; Gaps
                                                                                                                                                                                                                                                27 AFNLGA-GEKLLAYETSKKDPIVPFLLNLFLGFGI---GSFAQGDILGGFLILGFDAVGI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---FTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASAL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 451; 3.5;
                                                                                                                                                                                          71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                             Query Match 8.0%; Score ,2, ..., Best Local Similarity 21.3%; Pred. No. 3.5; Matches 37; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        us 08/679,635
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ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
STRAIN: RUSA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus aureus
STRAIN: RUSA 315
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Patent No. 6391614
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                                                                                                                                                                    -----AYLDGLAQQRRSDGLPATAVAWGTWAGSGMAEGAVADRFR 1804
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                                                                                                  23 AFKLGRYGGYVLAHNKGEKHP-----RVLVGRDTRVSGEMLESALIAGLISIGAEVMRL 76
                                                                     27 AFNLGA-GEKLLAYETSKKDPIVPFLLNLFLGFGI---GSFAQGDILGGFLILGFDAVGI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 61; Gaps
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                                           38;
                                                                                                                                                                                                                                            ----FTFANSYNRKLKNSLNIAFGGFEPSFDINMGQASAL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 3491;
Score 72; DB 4; Length 451;
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Katz, L
APPLICANT: Donadio, S
APPLICANT: Malpine, J B
TITLE OF INVENTION: Recombinant DNA Method for Producing
TITLE OF INVENTION: Erythromycin Analogs
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Abott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
                                     71;
ch 8.0%; Score 72; DB 4
1 Similarity 21.3%; Pred. No. 3.5;
37; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.8%; Score 70.5; Di 24.7%; Pred. No. 89; tive 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/07642734C Patent No. 5824513
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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Best Local Similarity 24.78
Matches 36, Conservative
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N: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
Query Match
Best Local Similarity
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                                                                                                                                                                                                                     131 IP----
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US-07-642-734C-2
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                                     Matches
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69 LGGFLILGFDAVGIGLILTGAYLDIKALDKNA---PKAAFKW-TWGKGMMLAGAVTMAVT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 3491;
                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Donadio, S
APPLICANT: Marz, L
APPLICANT: Moalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Steven F. Weinstock
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
| | | :| :| | 1:|:|: | 1805 RHGVIEMP---PETACRALQNALDRA 1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | || :|||| |
| 1739 LTAFVLFSSFASA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 RLTEIIIPFTFANSYNRKLKNSLNIA 150
                                                                                                                       Sequence 2, Application US/08439009A Patent No. 6004787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08608241 Patent No. 5747328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 49,
TELECOMMUNICATION INFORMATION:
TELECHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 24.7'
Matches 36; Conservative
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MOLECULE TYPE: protein
US-08-439-009A-2
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                             Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 60064-3500
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                                                                              RESULT 8
US-08-439-009A-2
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120 DGTSRFSMLDGTPILHYMGCSTFSNYTVLPEIAVAKVRPDAPFDKICYIGCGVTTGIGAV 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 HFVNPSEIDGDVVAHLVNMTKTPFDQIGGADYTFDCTGNVKVMRQALEACHRGWGQSIVI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 -SFAQGDILGGFLILGFDAVGI----GLILTGAYLDIKALDKNAPKAAFKWTWGK---- 111
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APPLICANT: Barber, Robert D
APPLICANT: Barber, Robert D
APPLICANT: Withhun, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: I South Pinckney Street
CITY: Madison
                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/922,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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23.0%; Pred. No. 5.3;
tive 26; Mismatches
                                                                                                                                                                                                                         NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93511
TELECOMMUTCATION INFORMATION:
TELEPHONE: 608-251-5000
TELEPRAX: 608-251-9166
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APPLICATION NUMBER: US/08/919,953
                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
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Patent No. 5837481
                                                                                                                                                                                                                                                                                                                          TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      376 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 23.0°
Matches 43; Conservative
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MOLECULE TYPE: protein

US-08-922-182-2
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CLASSIFICATION: 435
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                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                      FILING DATE:
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APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFTCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKEY NUMBER: 960296.93511
TELECOMMUNICATION INFORMATION:
TELECHONE: 608-251-9000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,241
                                    ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
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Patent No. 5834300
GENERAL INFORMATION:
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: 376 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-608-241-2
                     CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                              CITY: Madison STATE: WI
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                                                                                                                                        ZIP: 53703
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                                                                                                                       COUNTRY:
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146 SLNIAFGGFEPSF-----DINMGQASALGFELS 173
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NAME: Stuart, Donald R
REGESTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,608
TELECOMMUNICATION INFORMATION:
TELEFAN: (317)337-4816
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   Sequence 5, Application US/09036987A Patent No. 6143526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4928 amino acids
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Best Local Similarity 25.28
Matches 39; Conservative
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GY: linear
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                                                                                                                                                                295 GVAPAGA 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 -SFAQGDILGGFLILGFDAVGI----GLILTGAYLDIKALDKNAPKAAFKWTWGK---- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 INTAKVEIGAKAVVFGLGGIGLNVIQGLKLAGADMIIGVDLNNAKK-----EWGERFGMT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 ------GMMLAGAVTMAVTRLTEI-IIPFTFANSYNRK-LKNSLNIAFGGFEPSFDI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SFAQGDILGGFLILGFDAVGI----GLILTGAYLDIKALDKNAPKAAFKWTWGK---- 111
                                                                                                                                                                                                                                                                                                                                                                                            --ETSKKDPIVPFLLNLFLGFGIG----- 61
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FILE REFERENCE: 960296.95505
CURRENT APPLICATION NUMBER: US/09/192,983A
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/919,953
EARLIER PILING DATE: 1996-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 376
                                                                                                                                                                                                                                                                                                                         Length 376;
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23.0%; Pred. No. 5.3;
iive 26; Mismatches
                                                                                                         960296.93511
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09192983A Patent No. 6242244
                                               ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5006
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Rhodobacter sphaeroides
                                                                                                                                                        TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                               376 amino acids
                                                                                                                                                                                                                                                                                                                 Query Match 7.7%
Best Local Similarity 23.0%
Matches 43; Conservative
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acid
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APPLICANT: Donohue, Timothy
APPLICANT: Barber, Robert
APPLICANT: Witthuhn, Vernon
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Matches 43; Conservative
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                                                                                                                                                                                                                                                              // MOLECULE TYPE: protein
US-08-919-953-2
                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 GVAPAGA 301
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                                    FILING DATE:
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112 -----GMMLAGAVTMAVTRLTEI-IIPFTFANSYNRK-LKNSLNIAFGGFEPSFDI 160
               235 HFVNPSEIDGDVVAHLVNMTKTPFDQIGGADYTFDCTGNVKVMRQALEACHRGWGQSIVI 294
                                                                                                                                                         97 DKNAPKAAFKWTWGKGMMLAGAVTMAVTR-LIEII-----IPFTFANSYNR--KLKN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                    SSEE: Dow AgroSciences LLC Patent Department
P: 9330 Zionsville Road
Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.7%; Score 69.5; DB 4;
25.2%; Pred. No. 1.9e+02;
live 25; Mismatches 48;
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APPLICANT: DABAN, MONTSERRAT
APPLICANT: MEDRANO, ANDRES
APPLICANT: ESPUBA, ENRICUE
APPLICANT: ESPUBA, ENRICUE
TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEIN 1 (Tbp1) GENE OF
TITLE OF INVENTION: Actinobacillus pleuropneumoniae, ITS USE TO PREPA
TITLE OF INVENTION: PRODUCTS FOR THE UTILIZATION IN VACCINES FOR
TITLE OF INVENTION: PLEUROPNEUMONIA AND AS DIAGNOSTIC REAGENTS
TITLE OF INVENTION: PLEUROPNEUMONIA AND AS DIAGNOSTIC REAGENTS
FILE REFERENCE: P00740
CURRENT FILING DATE: 1996-03-22
PRIOR FILING DATE: 1995-03-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATCHIN VET: 2.1
SEQ ID NO 2
LENGTH: 931
                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Baltz, Richard H

APPLICANT: Broughton, Mary C

APPLICANT: Crawford, Kathryn P

APPLICANT: Treadway, Patt1 J

APPLICANT: Treadway, Patt1 J

APPLICANT: Turner, Jan R

APPLICANT: Waldron, Clive

TILLE OF INVENTION BLOSYNthetic Genes For Spinosyn Insecticide

FILE REFERENCE: 50489 DIV1

CURRENT FILING DATE: 1999-08-09

EARLIER FILING DATE: 1999-08-09

BARLIER FILING DATE: 1998-08-09

SOFTWARE: PAPLICATION NUMBER: US 09/36987

SOFTWARE: PAPLICATION VENCE: 200

SOFTWARE: PAPLICATION VENCE: 200

SOFTWARE: PAPLICATION VENCE: 200

SOFTWARE: PAPLICATION VENCE: 200

SOFTWARE: PAPLICATION VENCE: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.7%; Score 69.5; DB 4; Length 4928; Best Local Similarity 25.2%; Pred. No. 1.9e+02; Matches 39; Conservative 25; Mismatches 48; Indels 43
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2335 GLHSAFPVFADAFDEACCELDAHLGQMARLRDVLS 2369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Saccharopolyspora spinosa US-09-370-700-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/08624655A
; Patent No. 6323005
                                                                              RESULT 14
US-09-370-700-5
; Sequence 5, Application US/09370700
; Patent No. 6274350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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